Ulm, J.
09/899295 page 1
Seg. ID 2 w/ntext

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Database :
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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/cgn2_6/ptodata/1/paa/US06_C
/cgn2_6/ptodata/1/paa/US101_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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# ALIGNMENTS

US-09-791-537-57305; Application US/09791537

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GENERAL INFORMATION:

APPLICANT: Bionomix, Inc.

APPLICANT: Debe, Derek

APPLICANT: Debe, Derek

APPLICANT: Danzer, Joseph

TITLE OF INVENTION: METHODS OF USE THEREOF

FILE REFERENCE: 261/210

CURRENT FILING DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 153055

SOFTWARE: Patentin version 3.0

SEQ ID NO 57305

LENGTH: 359

TYPE: PRT

ORGANISM: Homo sapiens

US-09-791-537-57305

Ouery Match
Best Local Similarity 100.0%; Score 1860; DB 21; Length 359;
Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

MTLESIMACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLIGTGESGKSTFIKOMR 60

I MTLESIMACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKOMR 60

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NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.
SEQ ID NO 2
LENGTH: 359
TYPE: PRT
ORGANISM: Mus musculus
US-09-899-295-2
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US-09-471-572-8
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Sequence 8, Application US/09471572
GENERAL INFORMATION:
APPLICANT: Jones, Kenneth A.
APPLICANT: Walker, Mary W.
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APPLICANT: AVENILS Pharma Deutschland GmbH
TITLE OF INVENTION: Process for identifying
TITLE OF INVENTION: receptors
FILE REFERENCE: AVE D-2000/A033 englisch
CURRENT APPLICATION NUMBER: US/09/899,295
CURRENT FILING DATE: 2001-07-06
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Pred. No. 1.1e-175;
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RESULT 4
US-09-791-537-81282
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                                                                                                                                                                       NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 81282
LENGTH.
                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Bebe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: HTREE DIMENSIONAL STRUCTURES
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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CURRENT FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 359
                                                              Matches
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Best Local :
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APPLICANT: Branchek, Theresa A.
APPLICANT: Gerald, Christophe P.G.
TITLE OF INVENTION: Chimeric G-Proteins And Uses Thereof
FILE REFERENCE: 59896
                                                                                                                                                      LENGTH: 35
TYPE: PRT
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                                                                              Similarity
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Similarity 99.7%;
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                                                              Conservative
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Pred. No. 2.1e-175;
1; Mismatches 0;
                                                           Score 1857; DB 21;
Pred. No. 2.1e-175;
1; Mismatches 0;
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IIHGSGYSDEDKRGFTKLVYQNIFTAMQAMIRAMDTLKIPYKYEHNKAHAQLVREVDVEK

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APPLICANT: Jones, Kenneth A.

APPLICANT: Walker, Mary W.

APPLICANT: Branchek, Theresa A.

APPLICANT: Gerald, Christophe P.G.

TITLE OF INVENTION: Chimeric G-Proteins And Uses Thereof

FILE REFERENCE: 59996

FILE REFERENCE: 59996

CURRENT APPLICATION NUMBER: US/09/471,572

CURRENT FILING DATE: 1999-12-23

NUMBER OF SEQ ID NOS: 45

SOFTMARE: Patentin Ver. 2.1

SOFTMARE: Patentin Ver. 2.1
RESULT 6
US-09-791-537-78690
; Sequence 78690, A
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US-09-471-572-7
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 Application
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Pred. No. 1.3e-174;
1; Mismatches 1;
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APPLICANT: Bobomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 78690
LENGTH: 359
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Query Match
Best Local S
Matches 356
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SEQ ID NO 1
LENGTH: 359
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Best Local Similarity
Matches 357; Conserv
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                                                                                                                                                                                                                         TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS TITLE OF INVENTION: CHEMOSENSORY RECEPTORS FILE REFERENCE: 078003-140309
CURRENT APPLICATION NUMBER: PCT/US01/32619
CURRENT FILING DATE: 2002-09-20
                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/243,770 PRIOR FILING DATE: 2000-10-30 NUMBER OF SEQ ID NOS: 31
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                                                                                                      LENGTH: 35
TYPE: PRT
 Local Similarity
nes 356; Conserv
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Pred. No. 1.3e-174;
1; Mismatches 1;
Score 1846; DB 1;
Pred. No. 2.6e-174;
2; Mismatches 1;
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Sequence 1, Application PC/TUS0132819

Sequence 1, Application PC/TUS0132819

GENERAL INFORMATION:
APPLICANT: YAO, YONG
APPLICANT: XU, HONG
TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS
FILE OF INVENTION: CHEMOSENSORY RECEPTORS
FILE REFERENCE: 078003-0280649

CURRENT APPLICATION NUMBER: PCT/YUS01/32819

CURRENT FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: 60/243,770
PRIOR FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 359
TYPE: PRT
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DAQAAREFILKMFVDLNPDSDKIIYSHFTCATDTENIRFVFAAVKDTILQLNLKEYNLV
              DAQAAREFILKMFVDLNPDSDKIIYSHFTCATDTENIRFVFAAVKDTILQLNLKEYNLV
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99.2%;
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APPLICANT: YAO, YONG
APPLICANT: XU, HONG
APPLICANY: XU, HONG
TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE
TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF
TITLE OF INVENTION: CHEMOSENSORY RECEPTORS
FILE REFERENCE: 078003-0280649
CURRENT APPLICATION NUMBER: US/09/984,292
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 60/243,770
PRIOR APPLICATION WIMBER: 60/243,770
PRIOR FILING DATE: 2000-10-30
NUMBER: OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 359
TYPE: PRT
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US-09-984-292-1
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                                                                                                                                                                                                                                   Sequence 1, Application US/09989497
GENERAL INFORMATION:
APPLICANT: YAO, YONG
APPLICANT: XU, HONG
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 1
LENGTH: 359
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Best Local :
                                                              CURRENT APPLICATION NUMBER: US/09/989,497
CURRENT FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 09/984,292
PRIOR FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 60/243,770
PRIOR FILING DATE: 2000-10-30
                                                                                                                                                                   TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF TITLE OF INVENTION: CHEMOSENSORY RECEPTORS FILE REFERENCE: 078003-0280735
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Similarity 99.2%;
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Pred. No. 2
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APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
FITTLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF
FITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOPTWARE: Patentin version 3.0
SEQ ID NO 72283
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Sequence 72283, Application US/09791537

GENERAL INFORMATION:
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US-09-989-497-1
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TYPE: PRT
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Pred. No. 3.3e
3; Mismatches
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US-09-471-572-6
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 95492
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 359
TYPE: PRT
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GENERAL INFORMATION:
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Best Local S
                                                                                   APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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APPLICANT: Walker, Mary W.
APPLICANT: Walker, Joseph
APPLICANT: Branchek, Theresa A.
APPLICANT: Gerald, Christophe P.G.
TITLE OF INVENTION: Chimeric G-Proteins And
FILE REFERENCE: 59896
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99.2%;
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Pred. No. 4.1e-174;
1; Mismatches 2;
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Sequence 27, Application PC/TUS0132619
GENERAL INFORMATION:
APPLICANT: SENOMYX, INC.
TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGC TITLE OF INVENTION: CHEMOSENSORY RECEPTORS
FILE REFERENCE: 078003-140309
CURRENT APPLICATION NUMBER: PCT/US01/32619
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/243,770
PRIOR APPLICATION NUMBER: 60/243,770
PRIOR FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 27
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PCT-US01-32619-27
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PCT-US01-32619-27
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US-09-791-537-95492
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                                        VSAFENPYDAIKSLWNDPGIQECYDRRREYQLSDSTKYYLNDLDRVADPAYLPTQQDVL 180
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Pred. No. 6.5e-174;
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Pred. No. 4.1e-174;
1; Mismatches 2;
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APPLICANT: XU, HONG

APPLICANT: XU, HONG

TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE

TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS

TITLE OF INVENTION: CHEMOSENSORY RECEPTORS

FILE REFERENCE: 078003-0280649

CURRENT APPLICATION NUMBER: PCT/USO1/32819

CURRENT FILING DATE: 2002-03-07

PRIOR APPLICATION NUMBER: 60/243,770

PRIOR REPLICATION NUMBER: 60/243,770

PRIOR FILING DATE: 2000-10-30

NUMBER OF SEQ ID NOS: 42

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 37

LENGTH: 359

TYPE: PRT

ORGANISM: Homo Sapiens
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                 DAQAAREFILKMFVDLNPDSDKIIYSHFTCATDTENIRFVFAAVKDTIIQLNLKEVNLV 359
                                                                      ESDNENRMEESKALFRTITTY PWFQNSSVILFLNKKDLLEEKIMY SHLVDYFPEYDGPQR
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Search completed: June Job time: 319 secs 30, 2003, 16:24:41

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/cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
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US-09-4468-002-4
US-10-39-4416-2
US-10-39-448-002-2
US-10-414-797-20
US-10-319-416-7851
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49632, A
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5597, Ap
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2, Appli
13, Appl
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Sequence 11560, A	Sequence 9379, Ap	Sequence 9379, Ap	Sequence 9379, Ap	Sequence 11687, A	Sequence 14917, A	Sequence 8098, Ap	Sequence 8098, Ap	Sequence 14917, A	Sequence 14917, A	Sequence 23965, A	Sequence 3898, Ap	Sequence 6727, Ap	Sequence 12, Appl	Sequence 3381, Ap	Sequence 3377, Ap	Sequence 3383, Ap	Sequence 3379, Ap	Sequence 2, Appli

## ALIGNMENTS

Application US/10405027

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; ORGANISM: Homo sapiens US-10-405-027-3227
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TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: DS806pl
CURRENT APPLICATION NUMBER: US/10/405,027
CURRENT FILING DATE: 2003-04-07
PRIOR APPLICATION NUMBER: 60/3369,808
PRIOR FILING DATE: 2002-04-04
PRIOR FILING DATE: 2002-04-04
PRIOR APPLICATION UMBER: 60/376,175
PRIOR FILING DATE: 2002-04-30
NUMBER OF SEQ ID NOS: 5810
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SEQ ID NO 3227
LENGTH: 359
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301
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DAQAAREFILKMFVDLNPDSDKIIYSHFTCATDTENIRFVFAAVKDTILQLNLKEYNLV
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99.4%;
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Pred. No. 4.1e-183;
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CURRENT APPLICATION NUMBER: US/60/453,050
CURRENT FILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 82762
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10419
LENGTH: 359
TYPE: PRT
ORGANISM: Homo sapiens
US-60-453-050-10419
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APPLICANT: CARGILL, Michele APPLICANT: LUKE, May TITLE OF INVENTION: STENOSIS, METHODS OF FILE REFERENCE: CL001457
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Best Local Similarity 99.4
2002 357; Conservative
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: IAKOUBOVA, Olga
TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DET
FILE REFERENCE: CL001456
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CURRENT FILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 82762
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10419
LENGTH: 359
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{\tt MTLESIMACCLSEE} A KEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIK QMR
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                                       Conservative
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                                                   Score 1849; DB 7;
Pred. No. 4.1e-183;
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Pred. No. 4.1e-183;
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; Sequence 5597, Applic
; GENERAL INFORMATION:
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US-60-455-444-5597
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5597
LENGTH: 359
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Best Local (
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CURRENT FILING DATE: 2003-03-18
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               DAQAAREFILKMEVDLNPDSDKIIYSHETCATDTENIREVEAAVKDTILQLNLKEYNLV
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DAQAAREFILKMEVDLNPDSDKIIYSHETCATDTENIREVFAAVKDTILQLNLKEYNLV
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Pred. No. 4.1e-183;
1; Mismatches 1;
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US-60-465-241-5597
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CURRENT FILING DATE: 2003-04-23
NUMBER OF SEQ ID NOS: 258418
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 5597
LENGTH: 359
TYPE: PRT
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SOFTWARE: FastSEQ for
SEQ ID NO 10419
LENGTH: 359
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: BEGOVICH, Ann
                                                               Matches
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01466
CURRENT APPLICATION NUMBER: US/60/466,412
CURRENT FILING DATE: 2003-04-30
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                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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              MTLESIMACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMR
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                                                                            Score 1849; DB 7; Pred. No. 4.1e-183;
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Pred. No. 4.1e-183;
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LENGTH: 359
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cockett, Mark Ian TITLE OF INVENTION: Transgenic Rat FILE REFERENCE: 3655/1J046US2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 3:
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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                                                                                                                       RVRVPTTGIIEYPFDLQSVIFRMVDVGGQRSERRKWIHCFENVTSIMFLVALSEYDQVLV
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Conservative
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as well as :
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Pred. No. 1.4e
2; Mismatches
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1.4e-182;
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359

240

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DAQAAREFILKMEVDLNPDSDKIIYSHETCATDTENIREVEAAVKDTILQLNLKEYNLV

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RESULT 9
US-10-352-843-13
: Sequence 13, Application US/10352843
: GENERAL INFORMATION:
: APPLICANT: MOOTE, Lisa
: APPLICANT: Kopczynski, Jenny
: APPLICANT: Doberstein, Stephen
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PCT-US03-02452-13
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Best Local
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CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 60/352720
PRIOR FILING DATE: 2002-01-28
NUMBER OF SEQ ID NOS: 25
                                  APPLICANT:
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TITLE OF INVENTION: MOLECULES THAT MODULATE G(ALPHA)q ACTIVITY AND METHODS
TITLE OF INVENTION: TREATING URINARY INCONTINENCE
FILE REFERENCE: 5624-277-228
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APPLICANT: Kindt, Rac
APPLICANT:
                 APPLICANT:
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TYPE: PRT
ORGANISM: Artificial
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             Cockett, Mark
Ramanathan, Chandra
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Doberstein, Stephen
Lodge,
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Pred. No. 8.4e-180;
1; Mismatches 2;
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative sp.
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 49632
LENGTH: 387
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                                                                                                                                  ORGANISM: Homo sapiens US-09-724-676-49632
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US-09-724-676-49632;
Sequence 49632; Ap
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LENGTH: 353
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Best Local
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Best Local S
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PRIOR APPLICATION NUMBER: US 60/352720
PRIOR FILING DATE: 2003-01-27
NUMBER OF SEQ ID NOS: 25
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TITLE OF INVENTION: MOLECULES THAT MODULATE G(ALPHA)q
TITLE OF INVENTION: TREATING URINARY INCONTINENCE
FILE REFERENCE: 5624-277-999
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                                 MTLESIMACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMR
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                                                                 Conservative
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99.2%;
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                                                                                 Score 1687; DB 5
Pred. No. 3e-166;
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Pred. No. 8.4e-180;
1; Mismatches 2;
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RESULT 12
US-09-949-016-7853
US-09-949-016-7853, Application US/09949016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 49632, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD
ITILE OF INVENTION: Variants of alternative sp
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
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US-09-724-676A-49632
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US-09-724-676A-49632
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TYPE: PRT
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Similarity 89.4%;
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             POLYMORPHISMS IN KNOWN GENES ASSOCIATED
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; Pred. No. 3e-166;
23; Mismatches 15;
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CCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSGYS

Query Match Best Local Similarity Matches 288; Conserv

82.5%; ilarity 82.1%; Conservative

35;

Score 1535; DI Pred. No. 1.5e 35; Mismatches

1.5e-150; ches 28; DB 6;

Indels

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Length

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US-10-326-896-2
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
; ORGANISM: Mus musculus US-10-326-896-2
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 7853
LENGTH: 351
                                                  SEQ ID NO 2
LENGTH: 355
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APPLICANT: Qin Zhang
TITLE OF INVENTION: GNAl4 G-Protein Signaling |
TITLE OF INVENTION: Subunit Gene Disruptions,
TITLE OF INVENTION: Thereto
                                                                                        CURRENT APPLICATION NUMBER: US/10/326,896
CURRENT FILLING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                  FILE REFERENCE: R-696
                                  LENGTH: 35
TYPE: PRT
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; ORGANISM: Caenorhabditis elegans
PCT-US03-02452-12
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SOFTWARE: Patentin version 3.2
SEQ ID NO 12
LENGTH: 355
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: PCT/US03/02452
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 60/352720
PRIOR FILING DATE: 2002-01-28
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TITLE OF INVENTION: TREATING URINARY INCONTINENCE

TITLE OF INVENTION: TREATING URINARY INCONTINENCE
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APPLICANT: Kindt, Rac
APPLICANT: Kopczynski
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ENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLEEKIMYSHLVDYFPEYDGPQRDAQA
                                                              PTTGIIEYPFDLQSVIFRMVDVGGQRSERRKWIHCFENVTSIMFLVALSEYDQVLVESDN
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Doberstein, Stephen
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Lodge, Nicholas
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Search completed: June Job time : 52 secs
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SEQ ID NO 4982
LENGTH: 355
TYPE: PRT
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APPLICANT: Hinkle, Gregory
APPLICANT: Slater, Steven of
APPLICANT: Goldman, Barry of
APPLICANT: Chen, Xianfeng
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 81.3%; Score 1513; DB 6; Local Similarity 82.0%; Pred. No. 3e-148;
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Maximum DB seq length: 2000000000
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                                                Murine G-protein 6
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Mouse G protein al
Human G protein al
phCaR/JmGluR2*Gqi5
Human phCaR/JmGluR
pmGluR2/CaR*Galpha
                                                                                                                                                                            Description
                 Human pmGluR2-CaR*
pmGluR2/CaR*Galpha
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                                                                                                                                                                                                                                                                                                                                                              Mouse; G-protein coupled receptor modulator; G-protein 6q14myr;
signal transduction.
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## ALIGNMENTS

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pathways, useful potentially as therapeutic agents, by screening with	Identifying compounds that modify activity of signal transduction		N-PSDB; ABA97518.	WPI; 2002-148182/19.		Kostenis E;		(AVET ) AVENTIS PHARMA DEUT GMBH.		08-JUL-2000; 2000DE-1033353.		05-JUL-2001; 2001WO-EP07667.		17-JAN-2002.		WO200204665-A2.		Mus musculus.		פוקומו נומוופעתכנוטוו.

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                                              New G-alpha-q protein variants, useful for analyzing and discovering agonists or antagonists of chemoreceptors, such as G protein coupled receptors involved in sensing of tastants, olfactants or pheromones
                                                                                                                                                                 WPI; 2002-519234/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G_q protein; sensory signaling; chemoreceptor; tastant; olfactant;
pheromone; G protein alpha sub-unit; q family; G alpha q.
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                                                                                                                                                                                                                                                                                                                               30-OCT-2000; 2000US-243770P
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Pred. No. 3.6e-176;
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Pred. No. 4.4e:175;
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G_q protein;
pheromone; G
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                                                                                                                         07-OCT-2002
                                                                                                                                               ABG68584 standard; Protein;
                                                                                           sensory signaling; chemoreceptor; tastant; olfactant; protein alpha sub-unit; q family; G alpha q.
                                                                                                                        (first entry)
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24-OCT-2001; 2001WO-US32619 10-MAY-2002 WO200236622-A2 Mus musculus 30-OCT-2000; 2000US-243770P SENOMYX INC

WPI; 2002-519234/55

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pheromone; G
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99.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              exhibits increased promisculty relative to the corresponding G_q protein. The variant is used to identify a compound that modulates sensory signaling in sensory cells and to identify a compound that interacts with the G_q variant protein The G_q protein variant is useful for analysing and discovering agonists or antagonists of chemoreceptors, such as G protein coupled receptors involved in sensing of tastants, olfactants or pheromones. This is the amino acid sequence of a G protein alpha sub-unit q family (G alpha q) protein that can functionally coupled to sensory cell receptors such as taste GPCR's (G protein-coupled receptors) and olfactory GPCR's in an overly promiscuous manner.
                                         G-protein fusion receptor; CaR; calcium receptor; GluR; metabotropic glutamate receptor; GABABR; chimeric receptorgamma-aminobutyric acid receptor; allosteric modulator; spinal cord injury; epilepsy; ischaemia; hypoglycaemia; Alzheimer's disease; hyperparathyroidism; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention describes an isolated variant of a G_q protein, whi exhibits increased promiscuity relative to the corresponding G_q The variant is used to identify a compound that modulates sensory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
                                                                                                                                       phCaR/hmGluR2*Gqi5 fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New G-alpha-q protein variants, useful for agonists or antagonists of chemoreceptors,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yao
                            cognitive disorder.
                                                                                                                                                                                                                                        AAY49127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptors involved in sensing of tastants, olfactants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | I HGSGYSDEDKRGFTKLYYQNIFTAMQAMIRAMDTLKIPYKYEHNKAHAQLYREVDVEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MTLESIMACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMR
                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                                                    DAQAAREFILKMEVDLNPDSDKIIYSHFTCATDTENIREVFAAVKDTILQLNLKEYNAV
                                                                                                                                                                                                                                                                                                                                   DAQAAREFILKMFVDLNPDSDKIIYSHFTCATDTENIRFVFAAVKDTILQLNLKEYNLV
                                                                                                                                                                                                                                                                                                                                                                                                                                             VSAFENPYVDAIKSLWNDPGIQECYDRRREYQLSDSTKYYLNDLDRVADPAYLPTQQDVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MTLESIMACCLSEEAKEARRINDEIERQLRRDKRDARRELKLLLLGTGESGKSTFIKQMR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RVRVPTTGIIEYPFDLQSVIFRMVDVGGQRSERRKWIHCFENVTSIMFLVALSEYDQVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IIHGSGYSDEDKRGFTKLVYQNIFTAMQAMIRAMDTLKIPYKYEHNKAHAQLVREVDVEK
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                                                                                                                                                                          (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                      Protein;
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                                                                                                                                        construct protein sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 23;
L.4e-174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             analyzing and discovering such as G protein coupled
                                                                                        receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
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                                                            anoxia;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                 component, are used to assess function of the various domains and to identify compounds (e.g. allosteric modulators or antagonists) that act on these domains. The modulators are potentially useful for treating or preventing diseases associated with the receptors, e.g. stroke, head or spinal cord injury, epilepsy, ischaemia, hypoglycaemia, anoxia, Alzheimer's disease, hyperparathyroidism, osteoporosis, cognitive disorders and depression. Nucleic acid (II) that encodes (I) is used:
(I) for recombinant production of corresponding proteins; and (2) to produce cells used in screening for modulators. Use of CaR and mGluR domains allows presentation of GABABR domains, to a binding agent, in a form more like the natural domain structure compared with use of incomplete receptors, lacking one or more domains. By shuffling different domains, agents can be identified that affect particular domains of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to G-protein fusion receptors (I) comprising: (I) in the N to C direction, extracellular (ECD), transmembrane (TMD) intracellular (ICD) domains, each chosen independently from a CAR (calcium receptor), GluR (metabotropic glutamate receptor) and GABABR (gamma-aminobutyric acid receptor); (2) an optional linker attached to the C-terminus of ICD; and (3) a G-protein (GP) linked to ICD or the linker. (I), and recombinant chimeric receptors (CR) without the GP
                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              different
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Simin RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New G-protein fusion receptors and chimeras containing domains from different receptors, used to screen for modulators, potentially use e.g. for treating or preventing stroke or Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-APR-1999;
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                                                                                                                                                                                                                                                                                                           Similarity
DAQAAREFILKMEVDLNPDSDKIIYSHFTCATDTENIREVFAAVKDTILQLNLKEYNL 358
                                                                                                                                                       VSAFENPYVDAIKSLWNDPGIQECYDRRREYQLSDSTKYYLNDLDRVADPAYLPTQQDVL 180
                                                                                                                                                                                          MTLESIMACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMR
                                                                                       RVRVPTTGIIEYPFDLQSVIFRMVDVGGQRSERRKWIHCFENVTSIMFLVALSEYDQVLV 1157
                                                                                                     RVRVPTTGIIEYPFDLQSVIFRMVDVGGQRSERRKWIHCFENVTSIMFLVALSEYDQVLV 240
                                                                                                                                          VSAFENPYVDAIKSLWNDPGIQECYDRRREYQLSDSTKYYLNDLDRVADPAYLPTQQDVL
                                                                                                                                                                                                                                              MTLESIMACCLSEEAKEARRINDEIERQLRRDKRDARRELKLLLLGTGESGKSTFIKQMR
                                     ESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLEEKIMYSHLVDYFPEYDGPQR 1217
                                                  ESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLEEKIMYSHLVDYFPEYDGPQR 300
                                                                                                                                                                                                                                                                                                                                                 1276 AA;
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                                                                                                                                                                                                                                                                                             Score 1827; DB 20;
Pred. No. 4.3e-172;
2; Mismatches 3;
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Simin RT;
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The invention comprises G-protein fusion receptors - comprising extracellular, transmembrane and intracellular domains similar to CaR, mGluR or GABAB receptor sequences. The G-protein fusion receptors of the invention may also possess a linker joined to the carboxy terminus of the intracellular domain, and a G-protein joined to the linker. The G-protein fusion receptors of the invention are useful for identifying modulators of CaR, mGluR and GABABR for use in treating associated conditions. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transmembrane domain; int modulator identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    domain of the receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human phCaR/hmGluR2*Gqi5 fusion construct protein
                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid sequence was used in the production of
EŞDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLEEKIMYSHLVDYFPEYDGPQR
                                                                                                                                       MTLESIMACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMR
                                                             RVRVPTTGIIEYPFDLQSVIFRMVDVGGQRSERRKWIHCFENVTSIMFLVALSEYDQVLV
                                                                                RVRVPTTGIIEYPFDLQSVIFRMVDVGGQRSERRKWIHCFENVTSIMFLVALSEYDQVLV
                                                                                                                                                                                                                                                                                                          MTLESIMACCLSEEAKEARRINDEIERQLRRDKRDARRELKLLLLGTGESGKSTFIKQMR
                                                                                                                                                                                                                                                                 IIHGSGYSDEDKRGFTKLVYQNIFTAMQAMIRAMDTLKIPYKYEHNKAHAQLVREVDVEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1276 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                           98.2%;
98.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   comprises
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                                                                                                                                                                                                                                                                                                                                                                                    Score 1827; DB 23;
Pred. No. 4.3e-172;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful for identifying r
G-protein joined to the
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ar domain; CaR; mGluR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Busby
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1276;
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                                                                              CC (1) in the N to C direction, extracellular (ECD), transmembrane (TMM) and CC intracellular (ICD) domains, each chosen independently from a CaR CC (calcium receptor), GluR (metabotropic glutamate receptor) and GABABR CC (gamma-aminobutyric acid receptor); (2) an optional linker attached to the C-terminus of ICD; and (3) a G-protein (GP) linked to ICD or the CC linker. (I), and recombinant chimeric receptors (CR) without the GP CC component, are used to assess function of the various domains and to CC identify compounds (e.g. allosteric modulators or antagonists) that act CC identify compounds (e.g. allosteric modulators or antagonists) that act CC in these domains. The modulators are potentially useful for treating or preventing diseases associated with the receptors, e.g. stroke, head or CC spinal cord injury, epilepsy, ischaemia, hypoglycaemia, anoxia, CC Alpheimer's disease, hyperparathyroidism, osteoporosis, cognitive CC Alpheimer's disease, hyperparathyroidism, osteoporosis, cognitive CC disorders and depression. Nucleic acid (II) that encodes (I) is used: CC (1) for recombinant production of corresponding proteins; and (2) to CC produce cells used in screening for modulators. Use of CRR and mGluR CC domains allows presentation of GABABR domains, to a binding agent, in a CC domains allows presentation of shapar domains. By shuffling different CC domains, agents can be identified that affect particular domains of a receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  e.g.
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   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Fig 12; 255pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention relates to G-protein fusion receptors (I) comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1158
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      1394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0080671
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Busby JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GluR; head injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Garrett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1275
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Query Match

98 . 28;

Score

1827;

DВ 20;

Length 1394;

of CaR,

mGluR

and (

invention may also possess a linker joined to the carboxy terminus of the intracellular domain, and a G-protein joined to the linker. The G-protein fusion receptors of the invention are useful for identifying modulators of the invention are useful for identifying modulators

the

GABABR for use in treating associated conditions.

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RESULT 8
AAO15095
ID AAO1
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The invention comprises G-protein fusion receptors - comprising extracellular, transmembrane and intracellular domains similar to CaR, mGluR or GABAB receptor sequences. The G-protein fusion receptors of t
                                                                                                                                                                                                 Stormann T,
Simin RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                            modulator
                                                                Example 3; Fig 12; 168pp;
                                                                                                                                                                                                                                                                              03-OCT-2000;
                                                                                                                                                                                                                                                                                                            03-OCT-2001;
                                                                                                                                                                                                                                                                                                                                             11-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; G-protein fusion
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                                                                                                                                                                                                                                               (NPSP-) NPS
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                                                                                                l G-protein fusion mGluR and GABABR, in of the receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                            identification.
                                                                                                                                                                                                                                                                                                                                                                                                             Homo
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                                                                                                                                                                                                                                               PHARM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             domain;
                                                                                                                                                                                                                                                                                                                                                                                                          sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry;
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                                                                                                                                  receptor,
                                                                                                                comprises
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor;
                                                                English
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2; Mismatches 3;
                                                                                                                                                                                                               Storjohann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fusion construct protein.
                                                                                                                useful for identifying modulators of G-protein joined to the intracellula
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                                                                                                                                                                                                               LL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CaR;
                                                                                                                                                                                                               Busby
                                                                                                                                                                                                                                                                                                                                                                                                                                                             mGluR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             GABABR;
                                                                                                                                                                                                                 Garrett
                                                                                                                   intracellular
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DR WPI:
DR W-PS
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Best Local
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                                                                                                                                                                                                                                                               Stormann
Simin RT;
                                                                     New G-protein fusion receptors and chimeras containing domains from different receptors, used to screen for modulators, potentially useful e.g. for treating or preventing stroke or Alzheimer's disease \,
                                                                                                                                                                                  WPI; 1999-610995/52.
N-PSDB; AAZ31065.
                                                                                                                                                                                                                                                                                                                                                                                                                                               02-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gamma-aminobutyric acid receptor; allosteric modulator; antagonist;
spinal cord injury; epilepsy; ischaemia; hypoglycaemia; anoxia;
Alzheimer's disease; hyperparathyroidism; osteoporosis; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G-protein fusion receptor; CaR; calcium receptor; GluR; head injury; metabotropic glutamate receptor; GABABR; chimeric receptor; stroke;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-JAN-2000
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                          Example 1;
                                                                                                                                                                                                                                                                                                                                                                                             03-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-OCT-1999
                                                                                                                                                                                                                                                                                                                                          (NPSP-) NPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9951641-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cognitive disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pmGluR2/CaR*Galphai5+3Ala linker fusion construct protein sequence.
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                          Fig 12;
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                                                                                                                                                                                                                                                                                     Storjohann LL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (calcium receptor), Guna (metabotropic glutamate receptor) and GABABR (calcium receptor); (2) an optional linker attached to the C-terminus of ICD; and (3) a G-protein (GP) linked to ICD or the Component, are used to assess function of the various domains and to identify compounds (e.g. allosteric modulators or antagonists) that act on these domains. The modulators are potentially useful for treating or preventing diseases associated with the receptors, e.g. stroke, head or spinal cord injury, policepy, ischaemia, hypoglycaemia, anoxia, Alzheimer's disease, hyperparathyroidism, osteoporosis, cognitive disorders and depression. Nucleic acid (II) that encodes (I) is used: domains allows presentation of corresponding proteins; and (2) to produce cells used in screening for modulators. Use of CaR and mGluR domains allows presentation of GABABR domains, to a binding agent, in a form more like the natural domain structure compared with use of incomplete receptors, lacking one or more domains. By shuffling different domains, agents can be identified that affect particular domains of a
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                                                                                                                                              Human; G-protein fusion receptor; extracellular domain; transmembrane domain; intracellular domain; CaR; mGluR;
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(1) in the N to C direction, extracellular (ECD), transmembrane (TMD)
intracellular (ICD) domains, each chosen independently from a CaR
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Pred. No. 4.9e-172;
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Matches 353
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                                         Human; G-protein fusion receptor; extracellular domain; transmembrane domain; intracellular domain; CaR; mGluR;
                                                                                 Human ph2SPMGluR3-CaR*AAA*Gqi5
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Simin RT;
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Pred. No. 4.9e-172;
2; Mismatches 3;
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RESULT 12
AAY49131
ID AAY49
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AC AAY49
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DE mGluR
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention comprises G-protein fusion receptors - comprising extracellular, transmembrane and intracellular domains similar to CaR, mGluR or GABAB receptor sequences. The G-protein fusion receptors of the invention may also possess a linker joined to the carboxy terminus of the intracellular domain, and a G-protein joined to the linker. The G-protein
                                         07-JAN-2000
                                                                    AAY49131;
                                                                                              AAY49131 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             intracellular domain, and a G-protein joined to the linker. The G-protein fusion receptors of the invention are useful for identifying modulators of CaR, mGluR and GABABR for use in treating associated conditions. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 18; 168pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel G-protein fusion CaR, mGluR and GABABR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stormann T,
Simin RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-OCT-2000;
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              mGluR8/CaR*Galphaqi5 fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    domain of the receptor
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                                                                                                                                                                                                                                                                                                                                                                                                     61 IIHGSGYSDEDKRGFTKLVYQNIFTAMQAMIRAMDTLKIPYKYEHNKAHAQLVREVDVEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                RVRVPTTGIIEYPFDLQSVIFRMYDVGGQRSERRKWIHCFENVTSIMFLVALSEYDQVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                              MTLESIMACCLSEEAKEARRINDEIERQLRRDKRDARRELKLLLLGTGESGKSTFIKQMR
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                                                                                                                                                                                                                                                                                         RVRVPTTGIIEYPFDLQSVIFRMVDVGGQRSERRKWIHCFENVTSIMFLVALSEYDQVLV
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                                        (first entry)
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                                                                                               Protein;
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98.6%;
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                                                                                              1418
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               construct
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Pred. No. 4.9e-172;
2; Mismatches 3;
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G-protein joined to the
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              protein
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Query Match
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Matches 353
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                                                                                                                                                                                                                                                                                                    preventing diseases associated with the receptors, e.g. stroke, head or spinal cord injury, epilepsy, ischaemia, hypoglycaemia, anoxia, Alzheimer's disease, hyperparathyroidism, elepoporosis, cognitive disorders and depression. Nucleic acid (II) that encodes (I) is used: (1) for recombinant production of corresponding proteins; and (2) to produce cells used in screening for modulators. Use of CaR and mGluR domains allows presentation of GABABR domains, to a binding agent, in a form more like the natural domain structure compared with use of incomplete receptors, lacking one or more domains. By shuffling differer domains, agents can be identified that affect particular domains of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New G-protein fusion receptors and chimeras containing domains from different receptors, used to screen for modulators, potentially use e.g. for treating or preventing stroke or Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G-protein fusion receptor; CaR; calcium receptor; GluR; hea metabotropic glutamate receptor; GABABR; chimeric receptor; gamma-aminobutyric acid receptor; allosteric modulator; ant spinal cord injury; epilepsy; ischaemia; hypoglycaemia; ano Alzheimer's disease; hyperparathyroidism; osteoporosis; dep cognitive disorder.
                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                         Similarity
                                                                                                                                                      MTLESIMACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMR 60
                                                       VSAFENPYVDAIKSLWNDPGIQECYDRRREYQLSDSTKYYLNDLDRVADPAYLPTQQDVL
                                                                                                 IIHGSGYSDEDKRGFTKLVYQNIFTAMQAMIRAMDTLKIPYKYEHNKAHAQLVREVDVEK
RVRVPTTGIIEYPFDLQSVIFRMVDVGGQRSERRKWIHCFENVTSIMFLVALSEYDQVLV
                                          VSAFENPYVDAIKSLWNDPGIQECYDRRREYQLSDSTKYYLNDLDRVADPAYLPTQQDVL 1239
                                                                                                            IIHGSGYSDEDKRGFTKLVYQNIFTAMQAMIRAMDTLKIPYKYEHNKAHAQLVREVDVEK 120
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Pred. No. 5e-172;
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depression;
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RESULT 13
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                             mGluR or GABAB receptor sequences. The G-protein fusion receptors of the invention may also possess a linker joined to the carboxy terminus of the intracellular domain, and a G-protein joined to the linker. The G-protein
                                                                                                                                                                                                                                                                                                                                                                                                                     The invention of extracellular,
                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                             present
                                                                                                                                                                                                                                                                                                                     intracellular domain, and a G-protein joined to the linker. The G-protein fusion receptors of the invention are useful for identifying modulators of CaR, mGluR and GABABR for use in treating associated conditions. The proceeds a single said GABABR for use in treating associated conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example
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Simin RT;
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                                                                                                                                                                                      Local 353;
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                                                                                                                                              1 MTLESIMACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Fig 12; 168pp;
                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                             amino acid
VSAFENPYVDAIKSLWNDPGIQECYDRRREYQLSDSTKYYLNDLDRVADPAYLPTQQDVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the receptor
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                                                                                                                                                                                                                                                                         1418 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                  comprises G-protein fusion receptors - comprising transmembrane and intracellular domains similar to CaR,
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                                                                                                                                                                                                                                                                                                             sequence was used in
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                                                                                                                                                                                                                    98.2%;
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intracellular domain; CaR; mGluR;
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Pred. No. 5e-1
2; Mismatches
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G-protein joined to the
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                                                                                                                                                                                                                                                                                                           the production
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                                                                                                                                                       extracellular, transmembrane and intracellular domains similar to CaR, mGluR or GABAB receptor sequences. The G-protein fusion receptors of the invention may also possess a linker joined to the carboxy terminus of the intracellular domain, and a G-protein joined to the linker. The G-protein fusion receptors of the invention are useful for identifying modulators of CaR, mGluR and GABABR for use in treating associated conditions. The present amino acid sequence was used in the production of the invention.
                                                                                                                                                                                                                                                                             Disclosure; Fig 16; 168pp; English.
                                                                                                                                                                                                                                                                                                             Novel G-protein fusion receptor, useful for identifying m CaR, mGluR and GABABB, comprises G-protein joined to the demain of the receptor.
                                                                                                                                                                                                                                                                                                                                                          WPI;
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Simin RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human phmGluR8-CaR*AAA*G-alpha-qi5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAO15103 standard;
                                                                                                                                                                                                                                                   The invention comprises G-protein fusion receptors - comprising
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transmembrane domain;
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                          DAQAAREFILKMFYDLNPDSDKIIYSHFTCATDTENIRFVFAAVKDTILQLNLKDCGL 1417
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IIHGSGYSDEDKRGFTKLVYQNIFTAMQAMIRAMDTLKIPYKYEHNKAHAQLVREVDVEK
                                                    MTLESIMACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMR
                                                                                                                                                                                                                                                                                                       the receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      identification.
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                                                                             Score 1827; DB 23;
Pred. No. 5e-172;
2; Mismatches 3;
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                                                                        invention may also possess a linker joined to the carboxy terminus of the intracellular domain, and a G-protein joined to the linker. The G-protein fusion receptors of the invention are useful for identifying modulators of CaR, mclur and GABABR for use in treating associated conditions. The present amino acid sequence was used in the production of the invention.
                                                                                                                                            The invention comprises G-protein fusion receptors - comprising extracellular, transmembrane and intracellular domains similar to CaimGluR or GABAB receptor sequences. The G-protein fusion receptors of
                                                                                                                                                                                                Disclosure; Fig 16; 168pp; English.
                                                                                                                                                                                                                         Novel G-protein fusion CaR, mGluR and GABABR, domain of the receptor
                                                                                                                                                                                                                                                                              WPI; 2002-330170/36.
                                                                                                                                                                                                                                                                                                      Stormann T,
Simin RT;
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1044	1044	1045	1045	1045	1045	1045	1045	1046	1046	1048	1048	1049	1049	1052	1052	• 1052	1052
56.1	56.1	56.2	56.2	56.2	56.2	56.2	56.2	56.2	56.2	56.3	56.3	56.4	56.4	56.6	56.6	56.6	56.6
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US-09-442-349A-39	US-08-878-801-2	US-09-442-349A-56	US-09-442-349A-54	US-09-442-349A-50	US-09-442-349A-48	US-09-442-349A-37	US-09-442-349A-3	US-09-442-349A-38	US-09-442-349A-36	US-09-442-349A-12	US-09-442-349A-5	US-09-442-349A-13	US-09-442-349A-11	US-09-442-349A-18	US-09-442-349A-9	US-09-442-349A-7	US-09-442-349A-1
Sequence 39, Appl	Sequence 2, Appli	Sequence 56, Appl	Sequence 54, Appl	Sequence 50, Appl	Sequence 48, Appl	Sequence 37, Appl	Sequence 3, Appli	Sequence 38, Appl	Sequence 36, Appl	•	Sequence 5, Appli	Sequence 13, Appl	Sequence 11, Appl	Sequence 18, Appl	Sequence 9, Appli	Sequence 7, Appli	Sequence 1, Appli

## ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: Negulascu, Paul
APPLICANT: Offermanns, Stefan
APPLICANT: Simon, Melvin
CURRENT APPLICATION UMBER: US/08/878,801
CURRENT FILING DATE: 1997-06-19
EARLIER APPLICATION UMBER: US 60/020,234
EARLIER APPLICATION UMBER: US 60/020,234

EARLIER APPLICATION UMBER: US 60/020,234

EARLIER APPLICATION UMBER: US 60/020,334

EARLIER FILING DATE: 1996-06-21

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens US-08-878-801-4
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Best Local S
Matches 207
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Patent No. 6004808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 374
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                         EDKRGFTKLVYQNIFTAMQAMIRAMDTLKIPYKYEHNKAHAQLVREVDVEKVSAFENPYV 129
                    LKMFVDL-----NPDSD-------KIIYSHFTCATDTENIRFVFAAVKDTILQLNLKEYN
                                                                                                                                                           NEYCFSVKKTKLRIVDVGGQRSERRKWIHCFENVIALIYLASLSEYDQCLEENDQENRME
                                                                                                                                                                                IEYPFDLQSVIFRMVDVGGQRSERRKWIHCFENVTSIMFLVALSEYDQVLVESDNENRME
                                                                                                     ESKALFRTIITYPWFQNSSVILFLNKKDLLEEKIMYSHLVDYFPEYDGPQRDAQAAREFI
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LDMYARVYASCAEPQDGGRKGSRARRFFAHFTCATDTQSVRSVFKDVRDSVLARYLDEIN
                                                                              ESLALFSTILELPWFKSTSVILFLNKTDILEDKIHTSHLATYFPSFQGPRRDAEAAKSFI
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Pred. No. 7.7e-100;
5; Mismatches 88;
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GENERAL INFORMATION:
APPLICANT: Wong, Yung H
TITLE OF INVENTION: G Protein
FILE REFERENCE: M99/0101/US
CURRENT APPLICATION NUMBER: US/09/442,349A
CURRENT FILING DATE: 199-11-17
NUMBER OF SEQ ID NOS: 116
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 31
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US-09-442-349A-29
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                                                                                                                                                  Sequence 31, Application US/09442349A Patent No. 6462178
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CURRENT FILING DATE: 1999-11-17
NUMBER OF SEQ ID NOS: 116
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 29
LENGTH: 374
TYPE: PRT
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GENERAL INFORMATION:
APPLICANT: Wong, Yung H
TITLE OF INVENTION: G Protein
FILE REFERENCE: M99/0101/US
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Best Local Similarity
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; OTHER INFORMATION:
US-09-442-349A-21
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US-09-442-349A-21
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                                                                                                                                                                                                                           SEQ ID NO 21
LENGTH: 374
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                  Matches
                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 21, Application US/09442349A Patent No. 6462178
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Best Local Similarity
                                                                                                                                                                                                                                                                                                   FILE REFERENCE: M99/0101/US
CURRENT APPLICATION NUMBER: US/09/442,349A
CURRENT FILING DATE: 1999-11-17
RUMBER OF SEQ ID NOS: 116
                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wong, Yung
TITLE OF INVENTION: G
                                                                                                                                                                                                                                                                                        SOFTWARE:
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ORGANISM: Artificial Sequence
FEATURE:
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EERKGFRPLVYQNIFVSMRAMIEAMERLQIPFSRPESKHHASLVMSQDPYKVTTFEKRYA
                           EDKRGFTKLYYQNIFTAMQAMIRAMDTLKIPYKYEHNKAHAQLVREVDVEKVSAFENPYV 129
                                                                        CLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKOMRIIHGSGYSD
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; Pred. No. 2e-99;
57; Mismatches
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1.6e-99;
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; OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: chimera US-09-442-349A-23
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GENERAL INFORMATION:
APPLICANT: WONG, Yung H
TITLE OF INVENTION: G Protein
FILE REFERENCE: M99/0101/US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
SEQ ID NO 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 23, Application US/09442349A Patent No. 6462178
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Best Local Similarity
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CURRENT FILING DATE: 1999-11-17
NUMBER OF SEQ ID NOS: 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 374
TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                           LKMEVDL-----NPDSD------KIIYSHETCATDTENIREVFAAVKDTILQLNLKEYN 357
                                                                                                                                                                                                                                                                          AAMQWLWRDAGIRACYERRREPHLLDSAVYYLSHLERITEEGYVPTAQDVLRSRMPTTGI
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                                                                   Sequence 30, Application US/09442349A
Patent No. 6402178
GENERAL INFORMATION:
APPLICANT: Wong, Yung H
TITLE OF INVENTION: G PROTEIN
FILE REFERENCE: M99/0101/US
CURRENT APPLICATION NUMBER: US/09/442,349A
CURRENT FILING DATE: 199-11-17
NUMBER OF SED ID NOS: 116
SOFTWARE: Patentin Ver. 2.1
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US-09-442-349A-30
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US-09-442-349A-25
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SOFTWARE: Pate
SEQ ID NO 30
FMGTH: 374
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GENERAL INFORMATION:
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Best Local Similarity
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TITLE OF INVENTION: G Protein
FILE REFERENCE: M99/0101/US
CURRENT APPLICATION NUMBER: US/09/442,349A
CURRENT FILING DATE: 1999-11-17
NUMBER OF SEQ ID NOS: 116
SOFTWARE: Patentin Ver. 2.1
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ORGANISM:
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OTHER INFORMATION: chimera
US-09-442-349A-32
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; OTHER INFORMATION:
US-09-442-349A-30
                                                                                                                                                                                                                                      FILE REFERENCE: M99/0101/US
CURRENT APPLICATION NUMBER: US/09/442,349A
CURRENT FILING DATE: 1999-11-17
NUMBER OF SEQ ID NOS: 116
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 32
LENGTH: 374
                                                                                                                              Matches
                                                                                                                                                 Query Match
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--- rocal Similarity
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TITLE OF INVENTION: G Protein
FILE REFERENCE: M99/0101/US
                                                                                                                                                                                                      LENGTH: 374
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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                                LKMFVDL-----NDDSD-----KIIYSHFTCATDTENIRFVFAAVKDTILQLNLKEYN 357
                                                      EDKRGFTKLVYQNIFTAMQAMIRAMDTLKIPYKYEHNKAHAQLVREVDVEKVSAFENPYV
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57.18;
                                                                                                                         57.1%; Score 1062; 1
57.1%; Pred. No. 2e-1
tive 56; Mismatches
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Pred. No. 26
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SEQ ID NO 34
LENGTH: 374
TYPE: PRT
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; OTHER INFORMATION: Description of Artificial Sequence: G
; OTHER INFORMATION: chimera
US-09-442-349A-34
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LDMYTRMYTGCVDGPEGSNRNKETKEIYSHFTCATDTNNIQFVFQAVTDVIIQNNLKYIG
                          LKMFVDL-----NPDSD-----KIIYSHFTCATDTENIRFVFAAVKDTILQLNLKEYN
                                                                                          ESLALFGTILELPWFKSTSVILFLNKTDILEEKIPTSHLATYFPSFQGPKQDAEAAKRFI
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FILE REFERENCE: M99/0101/US
CURRENT APPLICATION NUMBER: US/09/442,349A
CURRENT FILING DATE: 1999-11-17
NUMBER OF SEQ ID NOS: 116
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 22
LENGTH: 374
TYPE: PRT
ORGANISM: Artificial Sequence
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LENGTH: 374
TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                APPLICANT: Wong, Yung H
TITLE OF INVENTION: G Prote:
FILE REFERENCE: M99/0101/US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/442,349A CURRENT FILING DATE: 1999-11-17
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SOFTWARE: PatentIn Ve
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WVENTION: G Protein
ENCE: M99/0101/US
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Pred. No. 2.5e-99;
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LENGTH: 374
TYPE: PRT
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TITLE OF INVENTION: G Protein
TITLE OF STRENCE: M99/0101/US
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IEYPFDLQSVIFRMVDVGGQRSERRKWIHCFENVTSIMFLVALSEYDQVLVESDNENRME
                                 AAMQWLWRDAGIRACYERRREFHLLDSAVYYLSHLERITEEGYVPTAQDVLRSRMPTTGI
                                                                                                EERKGFRPLVYQNIFVSMRAMIEAMERLQIPFSRPESKHHASLVMSQDPYKVTTFEKRYA
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57.1%;
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                                                                                                                                                                                                                              Score 1061; DB 4;
Pred. No. 2.5e-99;
66; Mismatches 87;
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CURRENT APPLICATION NUMBER: US/09/442,349A
CURRENT FILING DATE: 1999-11-17
NUMBER OF SEQ ID NOS: 116
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 33
LENGTH: 374
TYPE: PRT
ORGANTE:
RESULT 14
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FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: G protein
; OTHER INFORMATION: chimera
US-09-442-349A-33
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TITLE OF INVENTION: G P:
FILE REFERENCE: M99/010
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Pred. No. 2.5e-99;
6; Mismatches 87
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Artificial Sequence
FEATURE: OTHER INFORMATION: Description of OTHER INFORMATION: chimera
US-09-442-349A-26
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US-09-442-349A-28
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GENERAL INFORMATION:
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Best Local
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TITLE OF INVENTION: G Protein
FILE REFERENCE: M99/0101/US
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TITLE OF INVENTION: Grotein
FILE REFERENCE: M99/0101/US
CURRENT APPLICATION NUMBER: US/09/442,349A
CURRENT FILING DATE: 1999-11-17
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                                                                               LENGTH: 374
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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1640.134 Million cell updates/sec
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## ALIGNMENTS

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FILE REFERENCE: AVE D-2000/A033 englisch
CURRENT APPLICATION NUMBER: US/09/899,295
CURRENT FILING DATE: 2001-07-06
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 359
TYPP: nom
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; TYPE: PRT
; ORGANISM: Mus musculus
US-09-899-295-2
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: Sequence 2, Application US/09899295

: Patent No. US20020127601A1
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APPLICANT: Aventis Pharma Deutschland GmbH
TITLE OF INVENTION: Process for identifying
TITLE OF INVENTION: receptors
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Best Local Similarity
Matches 359; Conserv
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                   ESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLEEKIMYSHLVDYFPEYDGPQR 300
                                                                                                                  RVRVPTTGIIEYPFDLQSVIFRMVDVGGQRSERRKWIHCFENVTSIMFLVALSEYDQVLV 240
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ESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLEEKIMYSHLVDYFPEYDGPQR
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APPLICANT: YAO, YONG
APPLICANT: XU, HONG
TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AG
TITLE OF INVENTION: CHEMOSENSORY RECEPTORS
FILE REFERENCE: 078003-0280735
FULE REFERENCE: 078003-0280735
CURRENT APPLICATION NUMBER: US/09/989,497
CURRENT FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 09/984,292
PRIOR FILING DATE: 2001-10-29
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APPLICANT: YAO, YONG
APPLICANT: XU, HONG
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Best Local
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CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 60/243,770
PRIOR FILING DATE: 2000-10-30
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FILE REFERENCE: 078003-0280649
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SOFTWARE: PatentIn Ver. :
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pred. No. 2.7e-148;
2; Mismatches 1;
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SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 1
LENGTH: 359
TYPE: PRT
ORGANISM: Mus sp.
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                                                                                                                                                                                                                                           SEQ ID NO 37
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Best Local
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CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 60/243,770
PRIOR FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: YAO, YONG
APPLICANT: XU, HONG
TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN
TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTA
TITLE OF INVENTION: CHEMOSENSORY RECEPTORS
FILE REFERENCE: 078003-0280649
FILE REFERENCE: 078003-0280649
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PRIOR FILING DATE: 2000-10-30
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                                                                                                                                                                                                                               LENGTH: 359
                                                                                                                      Local Similarity 99.1 nes 356; Conservative
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            61 IIHGSGYSDEDKRGFTKLVYQNIFTAMQAMIRAMDTLKIPYKYEHNKAHAQLVREVDVEK 120
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                                                                                                                      Score 1842; DB 10;
Pred. No. 5.9e-148;
1; Mismatches 2;
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Pred. No. 2.7e-148;
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; ORGANISM: Homo sapiens US-09-989-497-37
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US-09-989-497-37
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Best Local
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APPLICANT: YAO, HONG
TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE
TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF
TITLE OF INVENTION: CHEMOSENSORY RECEPTORS
FILE REFERENCE: 078003-0280735
CURRENT FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US/09/989,497
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 09/984,292
PRIOR APPLICATION NUMBER: 60/243,770
PRIOR FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 42
COMMENTS TO THE TOWN OF THE TOW
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TYPE: PRT
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DAQAAREFILKMFVDLNPDSDKIIYSHFTCATDTENIRFVFAAVKDTILQLNLKEYNLV 359
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Pred. No. 5.9e-148;
1; Mismatches 2;
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FILE REFERENCE: 078003-0280735
CURRENT APPLICATION NUMBER: US/09/989,497
CURRENT FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 09/984,292
PRIOR FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 60/243,770
PRIOR FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
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APPLICANT: YAO, YONG
APPLICANT: XU, HONG
APPLICANT: XU, HONG
TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE
TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND AITITLE OF INVENTION: CHEMOSENSORY RECEPTORS
FILE REPERENCE: 078003-0280649
FULE REPERENCE: 078003-0280649
CURRENT APPLICATION NUMBER: US/09/984,292
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 60/243,770
PRIOR FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 42
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SEQ ID NO 15
LENGTH: 359
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Best Local
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                                                                                                                                                                                                                                                                                                                                 Sequence 15, Application US/09989497 Patent No. US20020143151A1
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APPLICANT: XU, HONG
TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE
TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONI
TITLE OF INVENTION: CHEMOSENGORY RECEPTORS
LENGTH: 3:
TYPE: PRT
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Pred. No. 1.6e
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1.6e-147;
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APPLICANT: YAO, YONG
APPLICANT: YAO, HONG
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APPLICANT: YAO, YONG
APPLICANT: YAO, YONG
TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGG
TITLE OF INVENTION: CHEMOSENSORY RECEPTORS
FILE REFERENCE: 078003-0280649
CURRENT APPLICATION NUMBER: US/09/984,292
CURRENT ETLING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 60/243,770
PRIOR FILING DATE: 2000-10-30
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US-09-984-292-9
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US-09-984-292-9
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                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 9
LENGTH: 359
                                                                                                                                                                                                                                                                Query Match
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SOFTWARE: PatentIn Ver. 2
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pred. No. 2.9e-146;
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Pred. No. 1.6e-147;
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; Patent NO. USZUUZULZO,
; GENERAL INFORMATION:
; APPLICANT: YAO, YONG
; APPLICANT: XU, HONG
; TITLE OF INVENTION: G
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US-09-989-497-9
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PRIOR FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
                                                                    Sequence 2, Application US Patent No. US20020128433A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 353;
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Best Local Similarity
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TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF
TITLE OF INVENTION: CHEMOSENSORY RECEPTORS
FILE REFERENCE: 078003-0280735
CURRENT APPLICATION NUMBER: US/09/989,497
CURRENT FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 09/984,292
PRIOR FILING DATE: 2001-10-29
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TYPE: PRT
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Pred. No. 2.9e-146;
2; Mismatches 4;
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G-ALPHA-Q

PROTEIN VARIANTS

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TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AN TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGGIVERY OF AGGIVERY OF AGGIVERY OF AGGIVER OF INVENTION: CLEMOSENSORY RECEPTORS FILE REFERENCE: 078003-0280735
CURRENT APPLICATION NUMBER: US/09/989,497
CURRENT FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 09/984,292
PRIOR APPLICATION NUMBER: 09/984,292
PRIOR APPLICATION NUMBER: 60/243,770
PRIOR APPLICATION NUMBER: 60/243,770
PRIOR FILING DATE: 2001-10-30
NUMBER OF SEQ ID NOS: 42
                                                                                         ; TYPE: PRT
; ORGANISM: Mus
US-09-989-497-2
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US-09-984-292-2
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                                                                                                                                                                  SOFTWARE: PatentIn Ver. SEQ ID NO 2
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                                  Query Match
Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/984,292

CURRENT FILING DATE: 2001-10-29

PRIOR APPLICATION NUMBER: 60/243,770

PRIOR APPLICATION NUMBER: 60/243,770

PRIOR FILING DATE: 2000-10-30

RUMBER OF SEQ ID NOS: 42
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pred. No. 5.1e-146;
2; Mismatches 1;
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                 Score 1819; DB 10;
Pred. No. 5:1e-146;
2; Mismatches 1;
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US-09-984-292-21
US-09-984-292-21
; Sequence 21, Application US/09984292
; Patent No. US20020128433A1
; Patent No. US20020128433A1
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LENGTH: 359
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Best Local Similarity
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APPLICANT: XU, HONG
APPLICANT: XU, HONG
TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE
TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS (
TITLE OF INVENTION: CHEMOSENSORY RECEPTORS
FILE REFERENCE: 078003-0280649
CURRENT APPLICATION NUMBER: US/09/984,292
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 60/243,770
PRIOR FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.1
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ESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLEEKIMYSHLVDYFPEYDGPQR 300
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Pred. No. 6.3e-146;
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APPLICANT: Stanton, Marty
APPLICANT: Epstein, David
APPLICANT: Hamaguchi, No. US20030087239Aluko
APPLICANT: Hamaguchi, No. US20030087239Aluko
APPLICATION: Target Activated Biosensor an
FILE REFERENCE: 23239-501
CURRENT APPLICATION NUMBER: US/09/952,680A
CURRENT FILING DATE: 2001-09-13
PRIOR APPLICATION NUMBER: 60/232,454
PRIOR FILING DATE: 2000-09-13
NUMBER OF SEQ ID NOS: 75
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US-09-952-680A-27
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TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGG
TITLE OF INVENTION: CHEMOSENSORY RECEPTORS
FILE REFERENCE: 078003-0280735
CURRENT APPLICATION NUMBER: US/09/989,497
CURRENT FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 09/984,292
PRIOR FILING DATE: 2001-10-29
PRIOR FILING DATE: 2001-0-29
PRIOR APPLICATION NUMBER: 60/243,770
PRIOR TILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.1
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US-09-989-497-21
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LENGTH: 359
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Pred. No. 6.3e-146;
1; Mismatches 5;
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US-09-984-292-16
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US-09-952-680A-27
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LENGTH: 353
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SEQ ID NO 27
LENGTH: 353
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                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: YAO, YONG
APPLICANT: YAO, HONG
APPLICANT: XU, HONG
TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE
TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONI
TITLE OF INVENTION: CHEMOSENSORY RECEPTORS
FILE REFERENCE: 078003-0280649
CURRENT APPLICATION NUMBER: US/09/984,292
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 60/243,770
PRIOR APPLICATION NUMBER: 60/243,770
PRIOR FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 42
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GTP-binding	RGFFO1	RGRT12	RGRTO2	RGFFO2	RGMSO2	S27013	S28159	A61031	RGHUI2	S24362	S27014	RGHUI3	I50238	RGHYO2	RGRT13	S28158
	GTP"bindin	GTP-binding	Gi2 protein	GTP-binding	GTP-binding	GTP-binding										

## ALIGNMENTS

A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-359 <STR>
A; Cross-references: GB: M55412; NID:g193501; PIDN:AAA63306.1; PID:g193502
A; Cross-references: GB: M55412; NID:g193501; PIDN:AAA63306.1; PID:g193502
C; Comment: The G proteins are a family of guanine nucleotide-binding proteins that re ains. The beta and gamma chains, required for GTPase activity, appear to be common to rase; it is specific for each type of G protein.
C; Superfamily: GTP-binding regulatory protein Gs alpha chain
C; Superfamily: GTP-binding regulatory protein Gs alpha chain
C; Keywords: GTP binding; heterotrimer; nucleotide binding; P-loop; signal transductio
F; 46-53/Region: nucleotide-binding motif A (P-loop)
F; 274-277/Region: GTP-binding NKXD motif
F; 52/Binding site: GTP (Lys) #status predicted
F; 183/Modified site: ADP-ribosylarginine (Arg) (by cholera toxin) #status predicted GTP-binding regulatory protein Gg alpha chain - mouse
N;Alternate names: guanine nucleotide binding protein Gg alpha chain; heterotrimeric
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1992 #sequence\_revision 31-Dec-1992 #text\_change 19-Jan-2001
C;Accession: A38414
R;Strathmann, M.; Simon, M.I.
Proc. Natl. Acad. Sci. U.S.A. 87, 9113-9117, 1990
A;Title: G protein diversity: a distinct class of alpha subunits is present in verteb
A;Reference number: A38414; MUID:91067657; PMID:2123549
A;Accession: A38414; MUID:91067657; PMID:2123549 1 MTLESIMACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKOMR Similarity MTLESIMACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMR Conservative 99.8%; 99.7%; Score 1857; Db 1, 1; Mismatches Length 359; Indels 0, Gaps 60

300

240 180

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RESULT 2
S71963
GTP-binding
                                  A; Molecule type: mRNA

A; Residues: 1-359 <SHA>

A; Cross-references: GB:U10502; NID:g505689; PIDN:AAA52189.1;

A; Cross-references: GB:U10502; NID:g505689; PIDN:AAA52189.1;

C; Superfamily: GTP-binding regulatory protein Gs alpha chain

C; Keywords: GTP binding; nucleotide binding; P-loop; signal t

F; 46-53/Region: nucleotide-binding motif A (P-loop)

F; 274-277/Region: GTP-binding NKXD motif

F; 52/Binding site: GTP (Lys) #status predicted

F; 183/Modified site: ADP-ribosylarginine (Arg) (by cholera to
                                                                                                                                                                                                                                                                                                                    RESULT 3
$45699
GTP-binding regulatory protein alpha chair
N;Alternate names: G-alpha-q protein
C;Species: Xenopus laevis (African clawed
C;Date: 10-Dec-1994 #sequence_revision 10-
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A;Title: Specificity of G-alpha(q) and G-alpha(11) gene A; Reference number: S71963; MUID:96433124; PMID:8836152
A; Accession: S71963
                                                                                                                                                                                                                                                            R;Shapira, H.; Way, J.; Lipinsky, FEBS Lett. 348, 89-92, 1994
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Best Local Sim!
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A; Residues: 1-359 < JOH>
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ribosylarginine (Arg)
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10-Nov-1995 #text_change
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A; Residues: 1-359 <MAU>
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 RVRVPTTGIIEYPFDLQSVIFRMVDVGGQRSERRKWIHCFENVTSIMFLVALSEYDQVLV
                                        VMTFEQPYVSAIKTLWNDPGIQECYDRRREYQLSDSAKYYLSDVDRIATPGYLPTQQDVL
                                                                                                              IIHGSGYSEEDKKGFTKLVYQNIFTAMQSMIRAMETLKILYKYEQNKANAVLIREVDVEK
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Best Local
Matches 34
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6; Mismatches 7;
turkey)
19-Mar-1997
                                    phospholipase C-activating G protein
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Rimaurice, D.H.; Waldo, G.L.; Morris, A.J.; Nicholas, R.A.; Biochem. J. 290, 765-770, 1993
A;Title: Identification of Galpha(11) as the phospholipase A;Reference number: S30359; MUID:93207527; PMID:8457205
A;Accession: S30359 RESULT 4

\$30359
GTP-binding regulatory protein G alpha chain,
GTP-binding regulatory protein G alpha chain,
N;Alternate names: phospholipase C-activating
C;Species: Meleagris gallopavo (common turkey)
C;Date: 19-Mar-1997 #sequence\_revision 19-MarC;Accession: \$30359; \$33360
C;Accession: \$30359; \$33360 F;46-53/Region: nucleotide-binding motif A (P-loop)
F;156-158/Region: GTP-binding SAK/L motif
F;274-277/Region: GTP-binding NKXD motif
F;52/Binding site: GTP (Lys) #status predicted
F;183/Modified site: ADP-ribosylarginine (Arg) (by A; Experimental source: erythrocytes C; Superfamily: GTP-binding regulatory protein Gs alpha C; Keywords: GTP binding; nucleotide binding; P-loop A; Molecule type: protein A; Residues: 78-92;121-132;158-180;253-256;307-312;339-345;355-359 Similarity MTLESIMACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMR Conservative GB:X73072; plood 91.9%; 90.3%; NID:g312254; PIDN:CAA51530.1; Score 1709; DB 2; Pred. No. 6.4e-116; 2; Mismatches 13; (by cholera toxin) Length Indels C-activating G-protein PID: g312255 0 #status predicted 60 0

120

60

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RESULT 6
RGMS11
GTP-binding regulatory protein G11 alpha chain - mouse
N;Alternate names: guanine nucleotide binding protein G11 alpha cha
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 19-C;Accession: B38414
R;Strathmann, M.; Simon, M.I.
Proc. Natl. Acad. Sci. U.S.A. 87, 9113-9117, 1990
A;Title: G protein diversity: a distinct class of alpha subunits is A;Reference number: A38414; MUID:91067657; PMID:2123549
A;Accession: B38414
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 5
$45700
G-alpha-Il protein - African clawed frog
C; Species: Xenopus laevis (African clawed frog)
C; Species: Xenopus laevis (African clawed frog)
C; Date: 10-Dec-1994 #sequence_revision 10-Nov-1995 #text_change
C; Accession: $45700
R; Shapira, H; Way, J; Lipinsky, D.; Oron, Y; Battey, J.F.
FBBS Lett. 348, 89-92, 1994
A; Title: Neuromedin B receptor, expressed in Xenopus laevis oocy
A; Reference number: $45699; MUID:94298961; PMID:8026589
A; Accession: $45700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:U10494; NID:g505687; PIDN:AAA52188.1; C;Superfamily: GTP-binding regulatory protein Gs alpha chain C;Keywords: GTP binding; nucleotide binding; P-loop E;46-53/Region: nucleotide-binding motif A (P-loop) F;274-277/Region: GTP-binding NKXD motif
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A; Residues: 1-359 <SHA>
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                                                                                   A;Cross-references: GDB:132587; OMIM:139313
A;Map position: 19p13.3-19p13.3
C;Superfamily: GTP-binding regulatory protein Gs alpha chain C;Keywords: GTP binding; heterotrimer; nucleotide binding; P: F;46-53/Region: nucleotide-binding motif A (P-loop)
F;274-277/Region: GTP-binding NKXD motif
F;52/Binding site: GTP (Lys) #status predicted
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                                                                         ;183/Modified
                                     Query Match
     Matches
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A; Residues: 1-359 <STR>
A; Cross-references: GB:M55411; NID:g193499; PIDN:AAA63305.1; PID:g193500
C; Comment: The G proteins are a family of guanine nucleotide-binding proteins. The beta and gamma chains, required for GTPase activity, appear to rase; it is specific for each type of G protein.
C; Superfamily: GTP-binding regulatory protein Gs alpha chain C; Keywords: GTP binding; heterotrimer; nucleotide binding; P-loop; signal F; 46-53/Region: nucleotide-binding motif A (P-loop)
F; 274-277/Region: GTP-binding NKXD motif
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                                                                                                                                                                                     RVRVPTTGIIEYPFDLQSVIFRMVDVGGQRSERRKWIHCFENVTSIMFLVALSEYDQVLV
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                                                                           ESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLEDKILHSHLVDYFPEFDGPQR
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Pred. No. 5.7e
28; Mismatches
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5.7e-114;
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A; Molecule type: mRNA A; Residues: 1-359 < JIAS A; Residues: 1-359 < JIAS A; Cross-references: GB:M69013; NID:g183690; PIDN:AAA58624.1; PID:g183691 C; Comment: The G proteins are a family of guanine nucleotide-binding proteins that ains. The beta and gamma chains, required for GTPase activity, appear to be common rase; it is specific for each type of G protein. C;Accession: A39394
R;Jiang, M.; Pandey, S.; Tran, V.T.; Fong, H.K.W.
Proc. Natl. Acad. Sci. U.S.A. 88, 3907-3911, 1991
A;Title: Guanine nucleotide-binding regulatory proteins
A;Reference number: A39394; MUID:91219481; PMID:1902575 C;Species: Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence\_revision 31-Dec-1992 A; Reference number: A; Accession: A39394 GTP-binding regulatory protein Gy alpha chain - human  $N; Alternate\ names:\ guanine\ nucleotide\ binding\ protein$ #text\_change GУ in retinal alpha chain; heterotrimeric 19-Jan-2001 pigment epithelial

Local

Similarity

90.4%; 89.1%;

Pred. Score 1681; Mismatches No.

6.7e-114;

16;

0;

Gaps

0

DB 1;

Length 359;

(by cholera toxin)

#status

predicted

P-loop;

signal

transductio

to

Conservative

site: ADP-ribosylarginine (Arg)

353

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J. Biol. Chem. 266, 12676-12681, 1991
A;Title: Identification of two novel GTP-binding protein A;Reference number: A40891; MUID:91286303; PMID:1905731 A;Accession: B40891
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A;Residues: 1-353 <NAK>
A;Residues: 1-353 <NAK>
A;Cross-references: GB:D90336; NID:g217567; PIDN:BAA14350.1;
A;Cross-references: GB:D90336; NID:g217567; PIDN:BAA14350.1;
C;Superfamily: GTP-binding regulatory protein Gs alpha chain
C;Keywords: GTP-binding; nucleotide binding; P-loop
F;40-47/Region: mcleotide-binding motif A (P-loop)
F;150-152/Region: GTP-binding SAK/L motif
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Species: Bos primigenius taurus (cattle)
Date: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          268-271/Region: GTP-binding NKXD motif
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hes 316;
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EFILKMFVDLNPDSDKIIYSHFTCATDTENIRFVFAAVKDTILQLNLKEYNLV
                                                                            RMEESKALFRIIITYPWFQNSSVILFLNKKDLLEEKIMYSHLVDYFPEYDGPQRDAQAAR
                                                                                                                                                                            TGIIEYPFDLQSVIFRMYDVGGQRSERRKWIHCFENVTSIMFLVALSEYDQVLVESDNEN
                                                                                                                                                                                                                     RYVSAIKTLWNDPGIQECYDRRREYQLSDSAKYYLTDVDRIATSGYLPTQQDVLRVRVPT
                                                                                                                                                                                                                                          PYVDAIKSLWNDPGIQECYDRRREYQLSDSTKYYLNDLDRVADPAYLPTQQDVLRVRVPT 186
                                                                                                                                                                                                                                                                                                    YSEEDKRGFTKLVYQNIFTAMQAMIRAMETLKILYKYEQNKANALLIREVDVEKVTTFEH
                                                                                                                                                                                                                                                                                                                      YSDEDKRGFTKLYYQNIFTAMQAMIRAMDTLKIPYKYEHNKAHAQLVREYDVEKYSAFEN 126
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                                                          RMEESKALFRTIVTYPWFQNSSVILFLNKKDLLEDKILHSHLVDYFPEFDGPQRDAQAAR
                                                                                                                                        TGIIEYPFDLENIIFRMVDVGGQRSERRKWIHCFENVTSIMFLVALSEYDQVLVESDNEN
                                                                                                                                                                                                                                                                                                                                                                                 MACCLSDEVKESKRINAEIEKQLRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGAG
                                                                                                                                                                                                                                                                                                                                                                                                                    MACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKOMRIIHGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPQAAREFILKMFVDLNPDSDKIIYSHFTCATDTENIRFVFAAVKDTILQLNLKEYNLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLEEKIMYSHLVDYFPEYDGPQR 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RVRVPTTGIIEYPFDLENIIFRMVDVGGQRSERRKWIHCFENVTSIMFLVALSEYDQVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RVRVPTTGIIEYPFDLQSVIFRMVDVGGQRSERRKWIHCFENVTSIMFLVALSEYDQVLV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VTTFEHQYVSAIKTLWEDPGIQECYDRRREYQLSDSAKYYLTDVDRIATLGYLPTQQDVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IIHGAGYSEEDKRGFTKLVYQNIFTAMQAMIRAMETLKILYKYEQNKANALLIREVDVEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IIHGSGYSDEDKRGFTKLVYQNIFTAMQAMIRAMDTLKIPYKYEHNKAHAQLVREVDVEK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1667; DB 2;
Pred. No. 6.7e-113;
3; Mismatches 14;
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            A; Molecule type: mRNA
A; Residues: 1-355 < MIL>
A; Residues: 1-355 < MIL>
A; Cross references: GBL M80631; NID:g193568; PIDN:AAA83222.
A; Cross references: GBL M80631; NID:g193568; PIDN:AAA83222.
R; Strathmann, M.; Wilkie, T.M.; Simon, M.I.
Proc. Natl. Acad. Sci. U.S.A. 86, 7407-7409, 1989
A; Title: Diversity of the G-protein family: sequences from A; Reference number: A33833; MUID:90017488; PMID:2508088
A; Accession: E33833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В Q
                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 00, 1007 June 1987. A; Title: Characterization of G-protein alpha subunits in A; Reference number: A41534; MUID:92052208; PMID:1946421 A; Accession: A41534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-355 < NAK>
A; Residues: 1-355 < NAK>
A; Cross-references: GB D90335; NID:g217565; PIDN:BAA14349.1;
C; Superfamily: GTP-binding regulatory protein Gs alpha chain C; Keywords: GTP binding; nucleotide binding; P-loop F:42-49/Region: nucleotide-binding mottif A (P-loop)
F:152-154/Region: GTP-binding SAK/L motif
E;270-273/Region: GTP-binding NKXD mottif
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A40891
GTP-binding protein GL1 alpha chain - bovine
GTP-binding protein GL1 alpha chain - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 27-Mar-1992 #sequence_revision 27-Mar-1992
                                                                                                                                                                                                                                                                                                                                         GTP-binding
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Best Local :
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hes 289;
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39; Conservative
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Pred. No. 1.4e-103;
3; Mismatches 29;
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A;Reference number: A40891; MUID:91286303; PMID:1905731
                                                                                            #text_change
PID:g217566
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                                                                                            02-Feb-2001
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                                                                          Nukada,
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DEDKRGFTKLYYQNIFTAMQAMIRAMDTLKIPYKYEHNKAHAQLVREVDVEKVSAFENPY CCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSGYS DEDRKGFTKLVYQNIFTAMQAMIRAMDTLKIQYVCEQNKENAQLIREVEVDKVSTLSRDQ CCLSAEEKESQRISAEIERQLRRDKKDARRELKLLLLGTGESGKSTFIKQMRIIHGSGYS IIEYPFDLQSVIFRMVDVGGQRSERRKWIHCFENVTSIMFLVALSEYDQVLVESDNENRM VEAIKQLWQDPGIQECYDRRREYQLSDSAKYYLTDIDRIAMPAFVPTQQDVLRVRVPTTG Indels 0; 355 Gaps 188 308 248 184 64 244 0

R;Wilkie, T.M.; Scherle, P.A.; Strathmann, M.P.; Slepak, V.Z.; Proc. Natl. Acad. Sci. U.S.A. 88, 10049-10053, 1991 ;Species: Mus musculus (house mouse)
;Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 02-Feb-2001;Accession: A41534; E33833 from the <u>;</u> five additional G-9 PID:g193569 Simon, class: expression м. т. alpha-subu

in

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RESULT 11
S34347
GTP binding regulatory protein Gq alpha chain - great pond snail
C;Species: Lymnaea stagnalis (great pond snail)
C;Accession: S65461; S34347
R;Knol, J.C.; Rammatsingh, S.; van Kesteren, E.R.; van Minnen, J.; Planta, Eur. J. Blochem. 230, 193-199, 1995
A;Title: Cloning of a molluscan G protein alpha subunit of the Gq class whia A;Accession: S65461; MUID:95324523; PMID:7601100
A;Accession: S65461
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A; Cross-references: GB:MG7616; NID:g193380; PIDN:AAA633 C; Superfamily: GTP-binding regulatory protein Gs alpha C; Keywords: GTP binding; nucleotide binding; P-loop F; 42-49/Region: nucleotide-binding motif A (P-loop) F; 152-154/Region: GTP-binding SAK/L motif F; 270-273/Region: GTP-binding NKXD motif
                 QΥ
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A; Residues: 1-353 < KNO>
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288; Conser
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PYVDAIKSLWNDPGIQECYDRRREYQLSDSTKYYLNDLDRVADPAYLPTQQDVLRVRVPT
                                                     YSDEDKRSHIKIYYQNIFMAMHAMIRAMDTLNIQYINPANRENGNMIRQIDYETYTTFDK
                                                                             YSDEDKRGFTKLVYQNIFTAMQAMIRAMDTLKIPYKYEHNKAHAQLVREVDVEKVSAFEN
                                                                                                                            MACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSG
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|LKLYQDQNPDKEKVIYSHETCATDTENIREVFAAVKDTILQLNLREFNLV
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                                                                                                                                                                                                                                                                                site: ADP-ribosylarginine (Arg) (by cholera toxin) #status
                                                                                                                                                                                                         Conservative
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binding regulatory protein Gs alpha chain
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82.1%;
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Pred. No. 1.4e-1
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Pred. No. 2.3e-103;
                                                                                                                                                                                                         Mismatches
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1.4e-102;
hes 36;
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C.Species: Caenorhabditis elegans
C.Jate: 20-Sep-1999 #sequence_revision
C.Accession: T15288
R.Gattung, S.; Goela, D.; Wilson, R.
submitted to the EMBL Data Library, May
                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position: 1
A; Introns: 40/1; 82/3; 155,
C; Superfamily: GTP-binding
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A; Map position: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-355 <GAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: A; Accession: T15288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, May 1997 A; Description: The sequence of C. elegans co
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C; Species: Caenorhabditis elegans
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AREFILKMEVDLNPDSDKIIYSHFTCATDTENIREVFAAVKDTILQLNLKEYNLV
                                                                                                                                     PTTGIIEYPFDLQSVIFRMVDVGGQRSERRKWIHCFENVTSIMFLVALSEYDQVLVESDN
                                                                                                                                                                                               ENPYVDAIKSLWNDPGIQECYDRRREYQLSDSTKYYLNDLDRVADPAYLPTQQDVLRVRV 184
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                                                          ENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLEEKIMYSHLVDYFPEYDGPQRDAQA
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82.0%; Pred. No. 8.7e-102;
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GTP-binding regulatory protein Gq alpha chain - nor C; Species: Loligo forbesi (northern European squid) C; Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995

northern

European

#text\_change 02-Feb-2001

13

C;Accession: R;Ryba, N.J.I

S33309

Findlay,

J.B

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RESULT 14
JN0115
GTP-binding regulatory protein dgg alpha
N;Alternate names: dgg protein
C;Species: Drosophila melanogaster
C;Date: 12-Feb-1993 #sequence_revision 1:
C;Accession: JN0115
R;Lee, Y.J.; Dobbs, M.B.; Verardi, M.L.;
                                                                                                       A;Cross-references: FlyBase:FBgn0004435
A;Introns: 40/1; 101/3; 153/2; 196/2; 239/3; 298/1; 334/1
C;Superfamily: GTP-binding regulatory protein Gs alpha chain
C;Keywords: alternative splicing; GTP binding; nucleotide binding; P-loo
E;1-360/Product: GTP-binding regulatory protein dgg alpha chain I #statu
F;1-297,333-360/Product: GTP-binding regulatory protein dgg alpha chain
                                                                                                                                                                                                                                             R:Lee, Y.J.; Dobbs, M.B.; Verardi, Neuron 5, 889-898, 1990
A:Title: dgq: a drosophila gene end A;Reference number; JN0115; MUID:9; A;Accession: JN0115
A;Molecule type: DNA
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A; Residues: 1-354 <RRYA
A; Residues: 1-354 <RRYA
A; Cross-references: EMBL:L10289
C; Superfamily: GTP-binding regulatory protein Gs alpha
C; Keywords: GTP binding; nucleotide binding; P-loop
F; 40-47/Region: nucleotide-binding motif A (P-loop)
F; 150-152/Region: GTP-binding SAK/L motif
F; 269-272/Region: GTP-binding NKXD motif
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A;Title: The molecular cloning of the squid (Loligo forbesi) visual Gq-alpha A;Reference number: S33309; MUID:93277493; PMID:8503868
A;Accession: S33309
A;Status: preliminary
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                 Score 1425.5;
Pred. No. 1.8
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                                                                              ESKALFRTIITYPWFQNSSVILFLNKKDLLEEKIMYSHLVDYFPEYDGPQRDAQAAREFI
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Score 1066; DB 2; Pred. No. 1.6e-69; Mismatches

Length Indels

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GTP-binding protein alpha-15 chain - mouse C;Species: Mus musculus (house mouse) C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change C;Accession: B41534 R;Wilkie, T.M.; Scherle, P.A.; Strathmann, M.P.; Slepak, V.Z.; SProc. Natl. Acad. Sci. U.S.A. 88, 10049-1053, 1991 A;Title: Characterization of G-protein alpha submits in the G-q A;Reference number: A41534; MUID:92052208; PMID:1946421 A;Accession: B41534
A;Molecule type: mRNÅ A;Residues: 1-374 <WIL>A;Residues: 1-374 <WIL>A;Cross-references: GB:M80632; NID:g193570; PIDN:AAA37713.1; A;Cross-references: GB:M80632; NID:g193570; PIDN:AAA37713.1; C;Superfamily: GTP-binding regulatory protein Gs alpha chain C;Keywords: GTP binding; nucleotide binding; P-loop F:49-56/Region: nucleotide-binding motif A (P-loop) F:49-56/Region: GTP-binding NKXD motif
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         GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd
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p23625 drosophila
p30678 mus musculu
088302 rattus norv
p30679 homo sapien
000743 emericella
p52206 canis famil
074227 cochliobolu
p04898 homo sapien
p10824 rattus norv
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074259 sporothrix
p38401 cavia porce
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O73819 xenopus lae
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P91950 homarus ame
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Result No.

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Database

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oryzias lat	cavia porce	homo sapien	gallus gall	mus musculu	rattus norv	cricetulus	cavia porce	homo sapien	xenopus lae	gallus gall	colletotric

## ALIGNMENTS

Title: Perfect score: Sequence:

Run on: OM protein -

Scoring table:

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EMBL; M55412; AAA63306.1; ALT_INIT.  PIR; A38414; RGMSQ. HSSP; P10824; 1BOF. MGD; MGI:95776; Gnaq. InterPro; IPR001019; Gprotein_alpha. Pfam; PF00503; G-alpha; 1. PRINTS; PR00318; GPROTEINA. ProDom; PD000281; Gprotein_alpha; 1. SMART; SM00275; G-alpha; 1. GTP-binding; Transducer; Multigene family; ADP-ribosylation; Palmitate; Lipoprotein. LIPID 3 PALMITTATE.	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	FUNCTION: ( INVOLVED AS SIGNALING SI	PALMITOYLATION.  PALMITOYLATION.  TISSUE-Brain;  MEDLINE-94043367; PubMed-8227063;  Medegaertner P.B., Chu D.H., Wilson P.T., Levis M.J., Bourne H.R.;  "Palmitoylation is required for signaling functions and membrane attachment of Gq alpha and Gs alpha.";  A. Biol. Chem. 268:25001-25008(1993).	[1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. TISSUE-Brain; MEDLINE-9106/657; PubMed-2123549; Strathmann M., Simon M.I.; "G protein diversity: a distinct class of alpha subunits is present in vertebrates and invertebrates."; Proc. Natl. Acad. Sci. U.S.A. 87:9113-9117(1990).	NANG. Musculus (Mouse). Mus musculus (Mouse). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI TaxID-10090;	9; 72-1991 (Rel. 18, Created) 77-1994 (Rel. 30, Last sequence updat 77-2001 (Rel. 40, Last annotation upone nucleotide-binding protein G(q),	JIT 1 _MOUSE STANDARD: PRT: 353 AA.

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RESULT 2
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Best Local
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                                                                                                  Johnson G.J., Leis L.A., Dunlop P.C.;

"Specificity of G alpha q and G alpha 11 gen and erythrocytes. Expressions of cellular didifferences.";
Biochem. J. 318:1023-1031(1996).

-i- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROFINOLYED AS MODULATORS OR TRANSDUCERS IN INVOLVED AS MODULATORS OR TRANSDUCERS IN SIGNALING SYSTEMS.

-i- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UN THE ALPHA CHAIN CONTAINS THE GUANINE NUCL-
-i- SIMILARITY: BELONGS TO THE G-ALPHA FAMIL-
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
Guanine nucleotide-binding protein G(q), al
                                                                                                                                                                                                                                                                Canis familiaris (Dog).
Fukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                 sequence from N.A.
medLine=96433124; PubMed=8836152;
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Mammalia; Eutheria;
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                                                           s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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99.7%;
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GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

ADP-RIBOSYL(1) (BY A

(BY SIMILARITY).
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Pred. No. 2.5e
1; Mismatches
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                                                                                                   COMPOSED OF 3 UNITS (ALPHA, BET)
THE GUANINE NUCLEOTIDE BINDING
HE G-ALPHA FAMILY. SUBFAMILY 3 (
                                                                                                                                                                                                                                                          Craniata; Vej
; Fissipedia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C41B2AC11C674C5F CRC64;
                                                                                                                                                                                                                                                                                                ion update)
G(q), alpha
                                                                                                                        OF 3 UNITS
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                                                                                                                                                                                                                                                                  Vertebrata;
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2.5e-130;
nes 0;
                                                                                                                                                                                    gene expression :
r differentiation
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S IN VARIOUS
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                                                 as
                              http://www.isb-sib
                                                                                                                                                                                                                                                          Canidae;
                                        Usage
                                                are no rest
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Canis.
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                                                                                                                                             PROTEINS) ARE TRANSMEMBRANE
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                                                                                                   ING SITE. 3 (G(Q)).
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n and species
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                               .ch/announce/
                                                                                                                         GAMMA).
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RESULT 3
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AC P
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                             GBQ_RAT
P82471;
16-OCT-2001
16-OCT-2001
16-OCT-2001
                                                                                                                                         Submitted [2]
                                                                                                                                                                                     Strotmann
"Rat G alp
TISSUE=Brain cortex;
MEDLINE=93081611; PubMed=1333286;
Lesch K.-P., Manji H.K.;
"Signal-transducing G proteins and modulation of alpha subunit gene of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIPID
NP_BIND
NP_BIND
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NP_BIND
MOD_RES
                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=10116;
                                                                                                                                                                                                                              TISSUE=Brain;
                                                                                                                                                                                                                                                     SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                        GNAQ.
                                                                                                                                                                                                                                                                                                                                                                                                             Guanine
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                                                                                                                     SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus
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HSSP; P10824; 1BOF.
InterPro; IPR001019; Gpro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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SM00275; G-alpha; 1.
nding; Transducer; Multigen;
                                                                                                                                                                                     alpha
                                                                                                                                                                                                                                                                                                                                                                                                        2001 (Rel. 40, Created)
2001 (Rel. 40, Last seg
2001 (Rel. 40, Last ann
nucleotide-binding pro
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                                                                                                                  74-229 FROM
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oa; Chordata;
ia; Rodentia;
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annotation update)
protein G(q), alpha
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PALMITATE (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
ADP-RIBOSYL[1] (BY ACT
(BY SIMILARITY).
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Pred. No. 9.
                                                                                                                                                                                                                                                                                                                   Craniata; Ver
Sciurognathi;
                           and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
      expression
                           antidepressant drugs:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         353
                                                                                                                                                                                                                                                                                                                                          Vertebrata; Euteleostomi;
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.9e-130;
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SIMILARITY).
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B.R., Lin K.,

Hughes M

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RESULT 4
GBQ_HUMAN
ID GBQ_HUMAN
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Best Local S
Matches 349
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SEQUENCE
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NP_BIND
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-i- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE INVOLVED AS MODULATORS OR TRANSDUCERS IN VARIOUS TRANSMEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L37294; AAB02848.1; HSSP; P10824; 1BOF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
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SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).

THE ALPHA CHAIN CONTAINS THE GUANINE NUCLEOTIDE BINDING SITE.

SIMILARITY: BELONGS TO THE G-ALPHA FAMILY. SUBFAMILY 3 (G(Q)).
                                                                                                                                                                                          241
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                                                                                                                                                                                                               RMEESKALFRIIITYPWFQNSSVILFLNKKDLLEEKIMYSHLVDYFPEYDGPQRDAQAAR
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353 AA;
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GTP (BY SIMILARITY).
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SIMILARITY).
'TN REF. 2)
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      P50148; Q13462; Q92471; Q15108; 01-OCT-1996 (Rel. 34, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Guanine nucleotide-binding protein G(q), alph GNAQ OR GAQ.
                                                                                                                                                                                                                                                                                                                                                     Thomas C.P., Dunn M.J., Mattera R.;
"Ca2+ signalling in K562 human erythroleukaemia cells: edimethyl sulphoxide and role of G-proteins in thrombin-thromboxane A2-activated pathways.";
Biochem. J. 312:151-158(1995).
ei-cunction: GOANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS)
                                           use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                             between the Swiss Institute of Bioinfi
the European Bioinformatics Institute.
                                                                                                                                                                      This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Signal-transducing G proteins and antidepressant drugs: modulation of alpha subunit gene expression in rat brain. Biol. Psychiatry 32:549-579(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Johnson G.J., Leis L.A., Dunlop P.C.;
"Specificity of G alpha q and G alpha 11 of and G erythrocytes. Expressions of cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen B., Leverette R.D., Schwinn D.A., Kwatra M. "Human G(alpha q): cDNA and tissue distribution. Biophys. Acta 1281:125-128(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dong Q., Shenker A., Way J., Haddad B.R., McBride W.O., Spiegel A.M., Battey J.; "Molecular cloning of human G aipha q cDNR localization of the G alpha q gene (GNAQ) pseudogene.":
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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MEDLINE=96077138; PubMed=7492305;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND TISSUE
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                                                                                                                                                                                                  SIGNALING SYSTEMS.
SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
THE ALPHA CHAIN CONTAINS THE GUANINE NUCLEOTIDE BINDING SITE.
TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN OVARY, PROSTATE,
TESTIS AND COLON.
SIMILARITY: BELONGS TO THE G-ALPHA FAMILY. SUBFAMILY 3 (G(Q)).
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                                                                                                                                              SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
      U40038;
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o the EMBL/GenBank/DDBJ
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pRINTS; PR00318; GPROTEINA.
PRODOM: PD000281; GProtein_alpha;
SMART; SM00275; G-alpha; 1.
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EMBL; L76256; AAB39498.1; ALT_INIT.
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HSSP; P10824; 1BOF.
            Xenopodinae; Xen
NCBI_TaxID=8355;
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EMBL; U10502; AAA5;
HSSP; P10824; 1BOF
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E -> K (IN REF. 2).
S -> T (IN REF. 2).
L -> V (IN REF. 2).
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01-NOV-1995 (Rel. 32, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Guanine nucleotide-binding protein, al
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ProDom; PD000281; Gprotein_alpha;
SMART; SM00275; G-alpha; 1.
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Biochem. J. 290:765-770(1993).
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Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                              InterPro;
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"Identification of G alpha 11 as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Maurice D.H., Waldo
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INVOLVED AS MODULATORS OR TRANSDUCERS
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Chordata; Crani
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Meleagrididae; Meleag
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                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                ProDom; PD000281; Gprotein_alpha; 1.
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MEDLINE=91286303; PubMed=1905731;
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Mammalia; Eutheria;
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GB11_BOVIN
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Pfam; PF00503; G-alpha;
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                        90.9%;
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
ADP-RIBOSYL[1] (BY ACTION OF CO
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                      1691;
No. 6
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cora; Bovoidea;
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                                                                SEQUENCE OF 244-337 FROM N.A.
TISSUE-Hematopoietic;
MEDLINE=96077138; PubMed=7492305;
Thomas C.P., Dunn M.J., Mattera R.;
"Ca2+ signalling in K562 human erythroleukaemia cells:
"Ca2+ signalling in K562 human erythroleukaemia cells:
thromboxide and role of G-proteins in thrombin-thromboxane A2-activated pathways.";
Biochem. J. 312:151-158(1995).
                                                                                                                                                                                                                                                               Liu S., Attix C., Andreise T., Trankheim M., Coefield J., Duarte S., Lucas S., Bruce R., Kronmiller B., Arellano A., Montgomery M., CKObayashi A., Olsen A.S., Carrano A.V.; Submitted (JUL-1998) to the EMBL/GenBank/DDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bai X.H.,
Submitted
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15-UIL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Counting nucleotide-binding protein G(Y), alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jiang M., Pandey S., Tran V.T., Fong H.K.W.; "Guanine nucleotide-binding regulatory prote epithelial cells."; Proc. Natl. Acad. Sci. U.S.A. 88:3907-3911(1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Retina;
MEDLINE=91219481;
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Homo sapiens (Human).
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Mammalia; Eutheria;
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Attix C., Andreise T
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                           MODULATORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=1902575;
S., Tran V.T., F
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Primates;
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                           NUCLEOTIDE-BINDING |
ATORS OR TRANSDUCERS
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o the EMBL/GenBank/DDBJ
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F00503; G-alpha; 1.
PR00318; GPROTEINA.
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                                                                                            DAQAAREFILKMFVDLNPDSDKIIYSHFTCATDTENIRFVFAAVKDTILQLNLKEYNLV
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                                                                                                                                        ESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLEEKIMYSHLVDYFPEYDGPQR
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89.7%;
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
ADP-RIBOSYL[1] (BY AC
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Pred. No. 8.2e-120;
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M -> I (IN REF. 2).

N -> H (IN REF. 4).

Y -> H (IN REF. 4).

DA -> EP (IN REF. 1).

L -> P (IN REF. 2).
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DD37176589E66046 CRC64;
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FEBS Let
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HSSP; P10824; 1BOF.
InterPro; IPR001019; Gprotein_alpha
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NCBI_TaxID=8355;
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16-OCT-2001 (Rel.
Guanine nucleotid
                                                                                                                                                                                                                                                                                                                  SEQUENCE
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"Neuromedin
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNALING SYSTEMS: ACTS AS AN ACTIVATOR OF PHOSPHOLIPASE C. SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA 6 GAMMA). THE ALPHA CHAIN CONTAINS THE GOANNINE NUCLEOTIDE BINDING SITE. SIMILARITY: BELONGS TO THE G-ALPHA FAMILY. SUBFAMILY 3 (G(O)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pira H., Way J., Lipinsky D., Oron Y., Battey J.F. Lett. 349:318-318(1994).
FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way find and the first transitions as long as its content.
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319; Conser
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2001 (Rel. 40, Last
nucleotide-binding
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ESDNENRMEESKALFRTIITYPWFQNSSVILFLNKKDLLEEKIMYSHLVDYFPEYDGPQR
                                                                                           VCTFEQPYVNAIKNLWSDPGIQECYDRRREYQLSDSTKYYLTDVDRISKPGYLPTQQDVL
                                                                                                                                                  IIHGSGYSEEDKKGFTKLVFQNIFTAMQSMIRAMETLKILYKYEQNKANAQVVREVDVEK
                                                                                                                                                                                                         MTLDSTMACCLSEEVKESKRINAEIEKQLRRDKKDSRRELKLLLLGTGESGKSTFIKQMR
                                        RVRVPTTGIIEYPFDLENIIFRMVDVGGQRSERRKWIHCFENVTSIMFLVALSEYDQVLV
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annotation update)
protein, alpha-11 subunit.
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
ADP-RIBOSYL[1] (BY ACT
SIMILARITY).
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Pred. No. 1.9e
25; Mismatches
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..9e-119;
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EMBL; U37413; AAB36839.1; -
EMBL; U37411; AAB36839.1; JU
EMBL; U37412; AAB36839.1; JU
EMBL; M57617; AAA330301.1; -
PIR; B30414; RGMS11.
PIR; B30833; B33833.
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P21278; Q61939;
Q1-MAY-1991 (Rel. 18, C
Q1-MAY-1991 (Rel. 18, I
16-CCT-2001 (Rel. 40, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWI
between
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"G protein diversity: a distinct class of alpha

in vertebrates and invertebrates.";

Proc. Natl. Acad. Sci. U.S.A. 87:9113-9117(1990)
                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=90017488; PubMed=2508088; Strathmann M., Wilkie T.M., Simon "Diversity of the G-protein family
                                            PRINTS; PR00318; GPROTEINA.
ProDom; PD000281; Gprotein_alpha; 1.
SMART; SM00275; G-alpha; 1.
                                                                                                               HSSP; P10824; 1BOF.
MGD; MGI:95766; Gnall.
InterPro; IPR001019; Gp
Pfam; PF00503; G-alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
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    Transducer;
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Multigene family; ADP-ribosylation. GTP (BY SIMILARITY).
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Sciurognathi;
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Best Local S
Matches 318
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16-OCT-2001
16-OCT-2001
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SEQUENCE
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NP_BIND
MOD_RES
                 EMBL;
                                                                          between the Swiss Institute of Bioinformat
the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
                                                                                                                                                                                                             Submitted (FEB-2000)
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Strotmann R.;
                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                            This
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                      FUNCTION: GUANINE NUCLEOTIDE-BINDING FROLEDA
INVOLVED AS MODULATORS OR TRANSDUCERS IN VAR
SIGNALING SYSTEMS.
SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS
THE ALPHA CHAIN CONTAINS THE GUANINE NUCLEOT
THE ALPHA CHAIN CONTAINS THE G-ALPHA FAMILY. S
                                                                                     SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss institute of Bioinformatics and the EMBL outstation - European Bloinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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P10824; 1E
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                                                  requires a license agreement (S
an email to license@isb-sib.ch).
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40, Last sequence update)
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40, Tast annotation, alpha-11
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Rodentia;
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GTP (BY SIMILARITY).
ADP-RIBOSYL[1] (BY ACTION C
(BY SIMILARITY).
K -> L (IN REF. 2).
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Pred. No. 3
                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
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Mismatches 13.
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A33D2D6C6C62F8D5
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                                                               (See http://www.isb-sib.ch/announce/
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                                                                            Usage
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RESULT 12
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ID GB14_AC P3840
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DT 01-OC
DT Guani
GN GNA14+
OS BOS t
OC Manma
OC Manma
OC MANMA
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RN [1]
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Best Local S
Matches 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GB14_BOVIN
P38408;
01-OCT-1994
01-OCT-1994
16-OCT-2001
                                      "Identification of two novel GTP-binding protein alpha-su lack apparent ADP-ribosylation sites for pertussis toxin.

J. Biol. Chem. 266:12676-12681(1991).

-I- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTINVOLVED AS MODULATORS OR TRANSDUCERS IN VARIOUS TRANSICUALING SYSTEMS.

-I- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, B THE ALPHA CHAIN CONTAINS THE GUANINE NUCLEOTIDE BINDITES SIGNALING SYSTEMS.
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                    This SWISS-PROT
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Bovidae; Bovinae; Bo
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sm00275; G-alpha; 1.
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(Rel. 30, Last sequence update)
(Rel. 40, Last annotation update)
leotide-binding protein, alpha-14
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205 209
274 277
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                entry is copyright.
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
ADP-RIBOSYL[1] (BY AC
(BY SIMILARITY).
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Pred. No. 1
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SMART; SM00275; G-alpha; 1.
GTP-binding; Transducer; Multigene; MP_BIND 42 49 GTP (B' NP_BIND 201 205 GTP (B' NP_BIND 270 273 GTP (B' NP_BIND 179 179 ADP-RI MOD_RES 179 179 ADP-RI
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or send an
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    J. Biol. Chem -!- FUNCTION:
                                           SEQUENCE FROM N.A.
MEDLINE-98344029; PubMed-9677362;
Shapira H., Amit I., Revach M., O
"Galphal4 and Galphaq mediate the
oocytes.";
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PRINTS; PR00318; GPROTEINA.
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Amphibia; Batrachia,
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                                                                                                                                                                                                              Xenopodinae;
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Pred. No. 2.1e-108;
3; Mismatches 29;
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P30677;
01-APR-1993 (Rel. 25, Create
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INVOLVED AS MODULATORS OR TRANSDUCERS IN VARIOUS TRANSMEMBRANE STGNALING SYSTEMS. ACTS AS AN ACTIVATOR OF PHOSPHOLIPASE C. MEDIATES RESPONSES TO TRYPSIN.
SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAME THE ALPHA CHAIN CONTAINS THE GUANINE NUCLECTIDE BINDING SITE. SIMILARITY: BELONGS TO THE G-ALPHA FAMILY. SUBFAMILY 3 (G(Q)).
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269
178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA;
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204
272
178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             82.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               r; Multigene family; ADP-ribosylation.
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
ADP-RIBOSYL[1] (BY ACTION OF CTX)
(BY SIMILARITY).
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                            43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1537;
No. 2.
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There are no restrictions on if
                                                                                                                                                                                                                                                                                                                                                                                                                                                               .5e-108;
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Created)

PRT;

355

AA

sequence update)
annotation update)
protein, alpha-14

subunit

Craniata; Vertebrata; | Sciurognathi; Muridae;

Euteleostomi; Murinae;

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• <sup>v</sup>
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Diversity of the G-protein family: sequences from fi
alpha subunits in the mouse.";
Proc. Natl. Acad. Sci. U.S.A. 86:7407-7409(1989).
-1- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G
INVOLVED AS MODULATORS OR TRANSDUCERS IN VARIOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NP_BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P10824; 1BOF.
MGD; MGI:95769; Gna14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A41534; A41534.
PIR; E33833; E33833.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M80631; AAA83222.1; EMBL; M57616; AAA63304.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strathmann M., Wilkie T.M., Simon M.I., "Diversity of the G-protein family: seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ptam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression in lines.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-92052208; PubMed-1946421;
Wilkie T.M., Scherle P.A., Strath
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001019; Gprotein_alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=90017488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wilkie T.M., Scherle P.A., Strathmann M.P., Slepak V.Z., Simon "Characterization of G-protein alpha subunits in the Gq class: expression in murine tissues and in stromal and hematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNALING SYSTEMS.

SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMP THE ALPHA CHAIN CONTAINS THE GUANINE NUCLEOTIDE BINDING SITE.

SIMILARITY: BELONGS TO THE G-ALPHA FAMILY. SUBFAMILY 3 (G(0)).
                                                                                                                                         185
                                                                 245
                                                                                                                                                                              189
                                                                                                                                                                                                                  125
                                                                                                                                                                                                                                                                                                                                                                                                                                         288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF00503; G-alpha; 1.
'S; PR00318; GPROTEINA.
'm; PD000281; Gprotein_alpha;
'; SM00275; G-alpha; 1.
                             309
                                                                                                                                                                                                                                                                                              65
                                                                                                                                                                                                                                                                                                                               69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                           VDAIKSLWNDPGIQECYDRRREYQLSDSTKYYLNDLDRVADPAYLPTQQDVLRVRVPTTG
                                                                                                                                                                                                                                                                                        CCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSGYS
                           ILKMFVDLNPDSDKIIYSHFTCATDTENIRFVFAAVKDTILQLNLKEYNLV
                                                                                                                                                                                                                                                                                                                                                                    CCLSAEEKESQRISAEIERHVRRDKKDARRELKLLLLGTGESGKSTFIKQMRIIHGSGYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     355 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Acad. Sci. U.S.A. 88:10049-10053(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transducer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=2508088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49
205
273
273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41522 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           82.5%;
82.1%;
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GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

ADP-RIBOSYL[1] (BY ACTION OF CT

(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                           35;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1535; DB 1;
Pred. No. 3.5e-108;
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Best Local S
Matches 291
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NP_BIND
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MOD_RES
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015975;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between the Swiss Institute or province. There are no rest
the European Bioinformatics Institute. There are no rest
the European Bioinformatics Institutions as long as its content
he he non-profit institutions as long as its content
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15-JUL-1998
16-OCT-2001
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                                                                                                                                                                                                                                            Local 291;
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Palmitate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00275; G-alpha;
GTP-binding; Transducer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00503; G-alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001019;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Moll Pectinoidea; Pectinidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Guanine nucleotide-binding protein G(q), alpha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "A novel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNALING SYSTEMS.

SIGNALING SYSTEMS.

SIDBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAM-
SUBUNIT: G PROTEINS THE GUANINE NUCLEOTIDE BINDING SITE.

THE ALPHA CHAIN CONTAINS THE G-ALPHA FAMILY. SUBFAMILY 3 (G(Q)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G INVOLVED AS MODULATORS OR TRANSDUCERS IN VARIOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration seen the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PD000281;
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                                                                                                                                                                                                                                                                                   Similarity
PYVDAIKSLWNDPGIQECYDRRREYQLSDSTKYYLNDLDRVADPAYLPTQQDVLRVRVPT
                                                                                                                                                                                       MACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Go-mediated
                                                                      YSEEDKRGFIKIVYQNIFMAMHSMIRAMDTIKISFEVADNEENAIMIRQVDYETVTTLDS
                                                                                         YSDEDKRGFTKLVYQNIFTAMQAMIRAMDTLKIPYKYEHNKAHAQLVREVDVEKVSAFEN
                                                                                                                                                               MACCLSEEAKEQKRINCEIEKELRKAKRDARRELKLLLLGTGESGKSTFIKQMRIIHGTG
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3 3 4 4 4 47 47 199 203 268 271 177 177
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(Rel. 36, Last sequence update)
(Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              yessoensis (Ezo giant scallop)
etazoa; Mollusca; Bivalvia; Pter
Pectinidae; Mizuhopecten.
                                                                                                                                                                                                                                                                                                                                                       ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  272:22979-22989(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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ta A., Ishikawa
                                                                                                                                                                                                                                                                                 82.3%;
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                                                                                                                                                                                                                                                                                                                                                       MW;
                                                                                                                                                                                                                                                           32;
                                                                                                                                                                                                                                                                                                                                                                          PALMITATE (BY SIMILARITY).
PALMITATE (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
ADP-RIBOSYL[1] (BY ACTION OF (BY SIMILARITY).
                                                                                                                                                                                                                                                                                   Score 1530;
Pred. No. 8
                                                                                                                                                                                                                                                           Pred. No. 8.2
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           353
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                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              scallop)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 restrictions
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                                                                                                                                                                                                                                                                                                                                                                                                     CTX)
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Q9bzb9 homo sapien
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P91955 limulus pol
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Q8r2x9 mus musculu
Q17386 caenorhabdi
Q9n192 octopus vul
Q8t6p8 mamestra br
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Q9nfz0 calliphora
Q9nfz0 calliphora
Q9nfz0 ralliphora
Q9nfz0 ralliphora
Q9nfz0 ralliphora
Q9nfz0 drosophila
Q9y207 hydra magni
Q9xzv4 geodia cydo
Q9i7c8 drosophila
Q9tu29 orytolagus
Q8tga3 leptosphaer
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45.8	45.9	45.9	46.0	46.2	46.2	46.2	46.3	46.4	46.7	46.8	46.9	47.0	47.0	47.0	47.4	47.4	47.5	47.5	47.6	47.6	47.7		48.0		48.2	48.2	48.2	48.3
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## ALIGNMENTS

d (MAR-2002) to the EMB 329284; AAG61117.1; 493896; AAM2610.1; 0824; 1BOF.; IPR001019; Gprotein_a 00503; G-alpha; 1. 000503; G-protein_a 1. 000275; G-alpha; 1. 359 AA; 42142 WW;		GNAQ. Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Mammaila; Eutheria; Primates; NCBI_TaxID=9606; [1] SEQUENCE FROM N.A. MEDLINE=98366208; PubMed=97008 Gabbeta J., Dhanasekaran N., F "G alpha q CDNA sequence from Thromb. Res. 91:29-32(1998).	SULT 1  BZB9 PRELIMINARY; PRT; ( O9BZB9 PRELIMINARY; PRT; ( O9BZB9; O1-JUN-2001 (TrEMBLrel: 17, Created) 01-JUN-2001 (TrEMBLrel: 21, Last ancount o1-JUN-2002 (T
L/GenBank/DDBJ databases.  1pha.  a; 1.  6F69C4F617DFA7C7 CRC64;	nBank/DDBJ databases.  R.S.; nding protein (G protein) alpha q	Craniata; Vertebrata; Euteleöstomi; Catarrhini; Hominidae; Homo. 50; 100 A.K.; human platelets.";	I; 359 AA.  ted) sequence update) annotation update) otide binding protein alpha q).

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Similar to g
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Q91X95;
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MGD; MGI-9766; Gnall.
InterPro; IPR001019; Gprotein_alpha.
Pfam; PF00503; G-alpha; 1.
PRODOM; PD000281; Gprotein_alpha; 1.
SEQUENCE 359 AA; 41930 MW; 74379
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                               RVRVPTTGIIEYPFDLENIIFRMVDVGGQRSERRKWIHCFENVTSIMFLVALSEYDQVLV
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
guanine nucleotide binding protein, alpha
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; 41930 MW; 7437912FF0BAC855 CRC64;
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Rodentia;
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Pred. No. 5.7e
29; Mismatches
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Pred. No. 3e-136;
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Sciurognathi; Muridae;
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5.7e-122;
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P91955;
01-MAY-1997 (TrEMBLrel. 03
01-MAY-1997 (TrEMBLrel. 20
01-MAR-2002 (TrEMBLrel. 20
03 protein alpha subunit.
Limulus polyphemus (Atlant:
Eukaryota; Metazoa; Arthrop
                  Q9U473;
Q9U473;
01-MAY-2000
01-MAY-2000
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"Molecular and Immunological Characterization of a Gq Protein from
Ventral and Lateral Eye of the Horseshoe Crab Limulus polyphemus.";

Invert. Neurosci. 0:0-0(1997).

EMBL; U88586; AAB48510.1; -.

HSSP; P10824; IBOF.

InterPro: IPR001019; Gprotein_alpha.
PFANTS; PF00503; G-alpha; 1.
PRINTS; PR00318; GPROTEINA.
PRINTS; PR000281; Gprotein_alpha; 1.
SMART; SM00275; G-alpha; 1.
SMART; SM00275; G-alpha; 1.
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                    (TrEMBLiel.
                                                                  PRELIMINARY;
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Arthropoda; Chelicerata;
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Pred. No. 1.8e
28; Mismatches
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1.8e-112;
hes 32;
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Matches 293
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EMBL; AF201328; AAF19378.1; -.

HSSP; P10824; LBOF.
                                                                                                                                                     Guanine nucrec.
Guanine nucrec.
Mus musculus (Mouse).
Mus musculus (Mouse).
Metazoa; Chordata;
Metazoa; Rodentia;
                                                                                                                                                                                                                                                                   O8R2X9;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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TISSUE-OLFACTORY ORGAN;
MEDLINE-20347127; PubMed=10781594;
MEDLINE-20347127; PubMed=10781594;
Strausberg R.; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases EMBL; BC027015; AAH27015.1; -. SEQUENCE 355 AA; 41527 MW; D34B39ACD179AE82 CRC64:
                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
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Panulirus argus (Spiny lobster).
Eukaryota, Metazoa; Arthropoda; Crustacea; Malac
Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
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                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YSDEDKRGFIKLVFQNIFMAMQSMIRAMDLLQISYGDSANIEHADLVRGVDYESVTTFEE
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Pred. No. 1.6e
24; Mismatches
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Sciurognathi;
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1.6e-111;
                                                                                                                                                                                                     Vertebrata; Euteleostomi;
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Best Local S
Matches 286
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O17386; O02546;
O1-NOV-1996 (TremBLrel. 01, C
O1-NOV-1996 (TremBLrel. 20, L
O1-MAR-2002 (TremBLrel. 20, L
EGL-30 (HETEROTRIMERIC G PROTEEL-30 OR MOLD7.7.
                                                                                                                                                                                             Watson
"2.2 M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                     Thierry-Mieg J., Thomas K., Vaudin M.,
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Simon M.I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
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                                                                                                                                                                                       on A., Weinstock I
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                                                                                                                               368:32-38(1994).
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protein alpha subunit).
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Pred. No. 6.6e
36; Mismatches
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                                                                                                                                                                                       Vaughan K., Wate oat J., Wohldman nce from chromosc
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Matches 291
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                                                                                                                                                                                                                                             09NL92;
01-OCT-2000
01-OCT-2000
01-MAR-2002
G protein a :
                                                                                                                                                                       Octopus vulgaris (Octopus).
Eukaryota; Metazoa; Mollusca; Cephalopoda;
Incirrata; Octopodidae; Octopus.
                         "G protein alpha subunit Submitted (APR-1999) to t
                                                        Iwasa T., Yanai T.,
Tsuda M.;
                                                                                                   TISSUE-EYE;
                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                     NCBI_TaxID=6645
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PRINTS; PR00318; GPR0TEINA.
ProDom; PD000281; Gprotein_alpha;
SMART; SM00275; G-alpha; 1.
SEQUENCE 355 AA; 41865 MW; FEZ
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6; Mismatches 36;
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PRINTS; PR00318; GPROTEINA.
PRODOM; PD000281; GPROTEINA. 1.
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R SMART; SM00275; G-alpha; 1.
R SMART; SM00275; G-alpha; 1.
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EMBL; AI
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Jacquin-Joly E., Francois
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Neoptera; Endopterygota; Lepidoptera; Glossata; Di
; Noctuidae; Hadeninae; Mamestra.
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Q8WSU8;
01-MAR-2002
01-MAR-2002
01-JUN-2002
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Eukaryota; Metazoa; Chordata; Urochordata;
Stolidobranchia; Pyuridae; Halocynthia.
MCBI_TaxID=7729;
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2.9e-104;
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RESULT 11
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Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
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Query Match
Best Local S
Matches 268
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InterPro; IPR001019; Gprotein_alpha.
Pfam; PF00503; G-alpha; 1.
PRINTS; PR00318; GPROTEINA.
PRODOm; PD000281; Gprotein_alpha; 1.
SMART; SM00275; G-alpha; 1.
SEQUENCE 353 AA; 41295 MW; FFF7997
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2000 (TrEMBLrel. 20, Last annotation update)
Guanine nuclectide-binding protein alpha subunit.
Calliphora vicina (Blue blowfly) (Calliphora erythrocephala).
Enkaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta,
Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Musco
Oestroidea; Calliphoridae; Calliphora.
NCBI_TaxID-7373;
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Schulz S., Huber A., Schwab K., Paulsen R.;
Schulz S., Huber A., Schwab K., Paulsen R.;
"A novel Ggamma isolated from Drosophila constitutes
protein gamma subunit of the fly compound eye.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databas
EMBL; AJ250443; CAB76453.1; ...
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YSDEDKRGFTKLVYQNIFTAMQAMIRAMDTLKIPYKYEHNKAHAQLVREVDVEKVSAFEN |||:|||:|| : | : | : | : | : | : : | : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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Pred. No. 1.4e
99; Mismatches
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1.4e-103;
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Nematoda; Chromadorea; inae; Caenorhabditis.

Rhabditida; Rhabditoidea;

(corresponding sequence M

M01D7

Created)

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Best Local Similarity
Matches 248; Conserv
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01-NOV-1999
01-MAR-2002
                                                  EMBL;
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MEDLINE=99246375; PubMed=10229568;
Suga H., Koyanagi M., Hoshiyama D.,
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                                                                                                                                                                                                                                                   NCBI_TaxID=6085;
                                                                                                                                                                                                                                                                                                       Hydra magnipapillata (Hydra).
Eukaryota; Metazoa; Cnidaria;
                                InterPro;
                                                                                                          tyrosine
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Gattung S., Goe
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1-MAR-2002 (TrEMBLrel. 20, Last
protein a subunit 3 (Fragment).
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osine kinases from sponge an
Mol. Evol. 48:646-653(1999).
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sequence of C. elegans
itted (MAY-1997) to the
                                                  AB006541;
P10824; 1B
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AF003739; AAM15593.1; -.
NCE 303 AA; 35807 MW; 12B5A76956116D:
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                              Gprotein_alpha
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12, Last sequence update)
20, Last annotation update)
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Q9XZV4;
01-NOV-1999
01-NOV-1999
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PRODOM; PD000281; Gprotein_alpha;
SMART; SM00275; G-alpha; 1.
NON_TER 1 1 1
SEQUENCE 305 AA; 35491 MJ.
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                                                                                                                                                                  ProDom; PD000281; Gprotein_alpha;
SMART; SM00275; G-alpha; 1.
SEQUENCE 355 AA; 41363 MW; 68:
                                                                                                                                                                                                                                InterPro; IPR001019; Gprote Pfam; PF00503; G-alpha; 1. PRINTS; PR00318; GPROTEINA.
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EMBL; Y14248; CAB43527.1;
HSSP; P04896; 1AZT.
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Po
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Astrophorida; Geodiidae;
NCBI_TaxID=6047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Geodia
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Local Sir
hes 221;
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Local Similarity 61.4%;
nes 215; Conservative 5
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ota; Metazoa; Porifera;
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21; Conservative
MSCLLSEEERLQKRINTRINKELQRDHKDAKKEIKLLLLGTGESGKSTFIKQMRIIHGKG
                            MACCLSEEAKEARRINDEIERHVRRDKRDARRELKLLLLGTGESGKSTFIKQMRIIHGSG
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Pred. No. 1.4e
51; Mismatches
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Q917C8;
01-MAR-2001 (TrEMBLrel. 1
01-MAR-2001 (TrEMBLrel. 1
01-JUN-2002 (TrEMBLrel. 2
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G-ALPHA-49B OR CG17759.
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Eukaryota; Metazoa; Arthropoda; Trac
Eukaryota; Neoptera; Endopterygota;
Ephydroidea; Drosophilidae; Drosophi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN-BERKELEY;
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eoptera; Endopterygota; Diptera; Brachycera; Musc
Drosophilidae; Drosophila.
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InterPro; IPR001019; Gprotein_alpha.
Pfam; PP00503; G-alpha; 1.
PRINTS; PR00318; GPROTEINA.
PRODOM; PD000281; Gprotein_alpha; 1.
SWART; SW00275; G-alpha; 1.
SEQUENCE 279 AA; 32844 MW; A9609C;
                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20035837; PubMed=10571060; Section 1.1.
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01-mAY-2000 (TrEMBLrel. 13,
01-mAY-2000 (TrEMBLrel. 13,
01-mAR-2002 (TrEMBLrel. 20,
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PRINTS; PR00318; GPROTEINA.
PRODOM; PD000281; Gprotein_alpha; 1.
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HSSP; P10824; 1AS3.
                                                                                                                                                                                                                                                                        "Cloning and characterization and mouse G(alpha)15."; FEBS Lett. 460:53-56(1999).
                                                                                                                                                                                                                                                                                                                                               Feild J.A., Foley J.J. Sarau H.M., Ames R.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9TU29
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                                                                                            SEQUENCE
                                                                                                               SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria;
                                                                                                                                                                                                      InterPro; IPR001019; Gprotein_alpha
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                                                                                                               SM00275; G-alpha; 1
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                                                                                            42933
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55.8%;
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Rubin
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    62;
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Score 1055; D. Pred. No. 2.7e 62; Mismatches
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G.M., Venter J.C.
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Search completed: June 30, 2003, 16:17:58 Job time: 83 secs